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RESULT 1
AAU04693
                                                                                                                                 August 2, 2004, 09:22:38 ; Search time 82.1053 Seconds (without alignments) 447.367 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                       Title:
Perfect score: 696
Sequence: 1 DTVPDNHRNKFKVINVDDDG......NNHQTELEVPRTPRTPTTPG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                1586107
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                     1586107 segs, 282547505 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Geneseq 29Jan04:*
1: geneseqp1980s:*
2: geneseqp200s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2003bs:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                         Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                          Run on:
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	Description	Human	Human			Aay07018 Breast ca		Aaw62507 p62 prote			Haemat		Human	Aam41592 Human pol	Human	062	6 Drosoj	7 Human	8 Human	Human	Aam39794 Human pol	76 Human	Add71132 Human int	580	10	Abg18438 Novel hum
	De	Aa	Ad	AP	Aa	Aa	æ	Вa	ΑĠ	겉	A	Æ	Aa	Aa	Aa	Aa	AP	Aa	Aa	Aa	Aa	Aa	A	A	Ag	¥
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SUMMARIES	D	AAU04693	ADC35101	ABB11822	AAW62558	AAY07018	ABB68120	AAW62507	ADD14099	ABG66871	AAY79184	ABR83336	AAM39806	AAM41592	AAM41593	AAB52062	ABB58836	AAM39807	AAM40528	AAM38742	AAM39794	AAB92876	ADD71132	AAM41580	AAG73503	ABG18438
	DB	4	7	4	0	7	4	7	7	Ŋ	m	9	4	4	41	٣	4	4	4	4	4	4	7	4	4	4
	Leng	508	508	N	508	101	442	481	509	541	359	331	337	365	365	412	622	252	315	306	326	326	338	371	365	473
о%	ery	100.0	100.0	100.0		56.2	'n.		20.6	ö	20.3				19.8	19.4		19.2	18.3	17.9	17.9			•	17.7	16.5
	Score	969	969	969	685	391	174	143.5	143.5	143.5	141		137.5	137.5	137.5	13	134.5		127.5	124.5	124.5	124.5	124.5	4	123.5	114.5
	Result No.		7	e	4	വ	9	7	00	6	10	TT.	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Aag75486 Human col	Abp41208 Human ova	Aao16354 Rat IRSAL	Abb60323 Drosophil	Abp53492 PTB domai	Aay13461 Amino aci		_	Abb99797 Amino aci	Abg72369 Human Ins	Human	Human	Abg72371 Human Ins	Human		Abb93323 Herbicida	Abg18131 Novel hum	Aao15273 Human ner	Adc31585 Human nov	Adc31584 Human nov
AAG75486	ABP41208	AA016354	ABB60323	ABP53492	AAY13461	AAW93972	AAB83921	ABB99797	ABG72369	ABG72372	ABG72370	ABG72371	ABG72368	ADA00642	ABB93323	ABG18131	AA015273	ADC31585	ADC31584
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289	268	1235	777	111	1242	1242	1242	1242	1242	1242	1242	1242	1242	1242	320	354	757	1094	111
16.0	13.7	11.8	11.6	11.2	11.2	11.2	11.2	11.2	11.2		11.2	11.2	11.2	11.2	10.8	10.8	10.8	10.8	10.8
111.5	95.5	82	80.5	~	78	78	7.8	78	78	78	78	78	78	78	'n	'n	75.5	75.5	75.5
26	27	28	5	30	31	32	33	34	35	36	37	38	3.9	40	41	42	43	44	45

ALIGNMENTS

	(first entry)
Human suc-1-a	suc-1-associated neurotrophic factor target protein (SNT-1).
Suc-1-associal	Suc-1-associated neurotrophic factor target protein; SNT-1;
protein co-ord	protein co-ordinate data; human; fibroblast growth factor receptor; nuclear magnetic resonance: NMR spectroscopy; rational drug design;
three-dimensional	onal structure.
Homo sapiens.	
Kev	Location/Oualifiers
Region	
	/note= "Beta sheet region #1"
Region	3540 /note_ mosts sheet region #0"
Region	more realis
	/note= "Beta sheet region #3"
Region	5257 /note= "Beta sheet region #4"
Region	6368 /note= "Reta sheet region #5"
Region	the real cases
Region	101601 20016
	/note= "Beta sheet region #7"
Region	99107 /note= "Alpha helix" [.]
Region	111115 /note= "Beta sheet region #8"
WO200151521-A2	2.
19-JUL-ZUUL.	
10-JAN-2001;	2001WO-US000821.
12-JAN-2000; 09-JAN-2001;	2000US-0175867P. 2001US-00757415.
TIMITOM (INTIOM)	SINAT SCHOOL MEDICINE.

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Gaps

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Indels

120

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Query Match
Best Local Similarity 100.
Matches 130; Conservative
      WPI; 2001-425868/45.
                                                                                                                                                                                                               WPI; 2003-829397/77.
N-PSDB; ADC35143.
                                                                Sequence 508 AA;
                                                                                                                                                                         US2003108888-A1.
                                                                                                                                               18-DEC-2003
                                                                                                                                                                                                        Scanlan MJ,
                                                                                                                                                                               12-JUN-2003
                                                                                                                                        ADC35101;
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                                                                                                                  131
                      Claim
                                                                                                                            RESULT 2
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The invention describes a method of diagnosing breast cancer in subject comprising contacting biological sample from subject with at least two different breast cancer-associated polypeptides (I) encoded by nucleic acid molecules (II) comprising sequence chosen from 42 fully defined sequences as given in specification, determining specific binding between (I) and agents in sample, where presence of the binding is diagnostic for breast cancer. The method is useful for diagnosing breast cancer in a subject. The sample is blood, lymph node fluid or breast discharge fluid. This is the amino acid sequence of a breast cancer antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 LFSFESGRKCQTGQGIFAFKCARAEELFNMLQEIMQNNSINVVEEPVVERNNHQTELEVP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human proteins and DNA encoding sequences useful for preventing, treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytokine; cell proliferation; cell differentiation; growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIVPDNHRNKFKVINVDDDGNELGSGIMELIDIELILYTRKRDSVKWHYLCLRRYGYDSN 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  namedopolesis regulation, tissue growth, immunomodulator; activin, inhibin; chemotaxis, chemokinesis, thrombolysis, oncogenesis; proliferation; metastasis, cancer; tumour; haematopoletic disorder; proliferation; arthritis; chronic inflammatory condition; proliferative retinopathy; arthritis; onnoic inflammatory condition; proliferative retinopathy; bone disorder; osteoporosis; vascular growth disorder; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; inflection; immune disorder; antiasthmatic; antiathritic; haemostatic; antiathritic; haemostatic; antiathritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human FGFR signalling adaptor SNT-1 homologue, SEQ ID NO:2192.
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                                                                                                                                                                                                                                                                                                              100.0%; Score 696; DB 7;
100.0%; Pred. No. 8e-75;
iive 0, Mismatches 0
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27-APR-2000; 2000US-00560875.
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Best Local Similarity 100.
Matches 130; Conservative
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N-PSDB; ABA09066.
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                                                                                                                                                                                                                                                                  Sequence 508 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence represents the amino acid sequence of human suc-1-associated neurotrophic factor target protein (SNT-1). The invention provides fragments of SNT and fibroblast growth factor receptor (FGFR) which form a binding complex that is amenable to structural determinations by muclear magnetic resonance (NMR) spectroscopy. The invention provides methodology for related structure based rational drug design using the three-dimensional data. The invention fulfills the need for the determination of the three-dimensional structure of such complexes as described and for procedures for related structureal base drug design predicated on such structural data
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 LFSFESGRRCQTGQGIFAFKCARAEELFNMLQEIMQNNSINVVEEPVVERNNHQTELEVP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 LFSFESGRRCQTGQGIFAFKCARAEELFNMLQEIMQNNSINVVEEPVVVERNNHQTELEVP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIVPDNHRNKFKVINVDDDGNELGSGIMELTDTELILYTRKRDSVKWHYLCLRRYGYDSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DTVPDNHRNKFKVINVDDDGNELGSGIMELTDTELILYTRKRDSVKWHYLCLRRYGYDSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                       New isolated nucleic acid sequences encoding polypeptides useful in
structure based rational drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 696; DB 4; Length 508; 100.0%; Pred. No. 8e-75; ive 0; Mismatches 0; Indels
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                                                                                                                                                                7; Page 228-230; 235pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human breast cancer antigen seg id 67.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADC35101 standard; protein; 508
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Sequences ABB19381-ABB12310 represent 1350 novel human polypeptides, and sequences ABB19381-ABB12310 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the nucleotides.

CC antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which cor polypeptides of the invention. Although novel, many of the which polypeptides of the invention have homology to known proceins, thereby giving an insight into their probable biological activities, and hence complications activities; including cytokine, cell proliferation or cell ferentiation activities; including cytokine, cell proliferation or cell mannomodulatory activity; tissue growth activity; chemological activities; nemotocial activities may be used to promote wound are activities may be used in the treatment of viral, becreail and fungal infections includes with activities may be used to convected and inductory activities may be used not polypeptid ameliorating a medical condition in a mammalian subject e.g. arthritis screening techniques. The present sequence represents a novel human polypeptide of the invention Claim 20; Page 261; 1963pp; English. screening

Sequence 521 AA;

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LFSFESGRRCQTGQGIFAFKCARABELFNMLQEIMQNNSINVVEBPVVERNNHQTELEVP 143
                                                                                                                                 LFSFESGRRCQTGQGIFAFKCARABELFNMLQEIMQNNSINVVEEPVVERNNHQTELEVP 120
                                                                     9
                                                                                                    83
                                                                                             DIVPDNHRNKFKVINVDDDGNELGSGIMELTDTELILYTRKRDSVKWHYLCLRRYGYDSN
                                                               DIVPDNHRNKFKVINVDDDGNELGSGIMELTDTELILYTRKRDSVKWHYLCLRRYGYDSN
                                    0
 100.0%; Score 696; DB 4; Length 521; 100.0%; Pred. No. 8.3e-75; ive 0; Mismatches 0; Indels (
                                    Conservative
                                                                                                                                                                                                 RIPRIPITIG 130
                                                                                                                                                                                                                              RTPRTPTTPG 153
Query Match
Best Local Similarity
                                130;
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AAW62558 standard; peptide; 508 AA. (revised) (first_entry) 25-MAR-2003 25-SEP-1998 AAW62558; AAW62558 RESULT XEXHEXEX

AAY07018 standard; protein; 101 AA.

RESULT 5
AAY07018
ID AAY0
XX

Fibroblast growth factor receptor protein kinase substrate 2 (FRS2).

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The present sequence represents an adaptor protein linking protein kinases to activating partners in cells. The protein is designated fibroblast growth factor receptor protein kinases substrate 2 (FRS2). It requilates the growth factor protein of cellular differentiation and cellular proliferation by linking stimulated fibroblast growth factor receptor to the Rass/MAPK cascade via Grb-2/Sos complex. The FRS2 protein is useful to diagnose abnormal conditions associated with cell proliferation or cell differentiation in organisms caused by an aberration in a signal transduction pathway characterised by an interaction between a FRS2 plyperide and a natural binding partner (especially in mammals). Such abnormal conditions can be associated with cell proliferation or cell differentiation. The protein is also useful to identify compounds that enhance or block FRS2 interactions with natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human adaptor protein FRS2 - useful in, e.g. diagnosis, prevention or treatment of abnormal conditions associated with cell proliferation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                partners, to diagnose, prevent or treat abnormal conditions. d on 25-MAR-2003 to correct PA field.) (updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 DTVPDNHRNKFKVINVDDDGNELGSGVMELTDTELILYTRKRDSVKWHYLCLRRYGYDSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Adapter protein; regulation; growth factor stimulation; fibroblast growth factor receptor protein kinase substrate 2; FRS2; cellular differentiation; cellular proliferation; stimulated fibroblast growth factor receptor; Ras/MAPK cascade; Grb-2/SoS complex; diagnosis; prevention; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                        /note= "phosphotyrosine binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                     Schlessinger J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.4%; Score 685; DB 2; L
Larity 97.7%; Pred. No. 1.7e-73;
Conservative 3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Lax I,
                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                              UYNY-) UNIV NEW YORK MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Fig 1A; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Kouhara H, Spivakkroizman T,
                                                                                                                                                                                                                                                                                                     97WO-US021851
                                                                                                                                                                                                                                                                                                                                         96US-0032093P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell differentiation.
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ses 127; Conserv
                                                                                                                                                                                                                                                                                                                                                                              (SUGE-) SUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 508 AA;
                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                     01-DEC-1997;
                                                                                                                                                                                                                                                                                                                                         3-DEC-1996;
                                                                                                                                                                                                                           WO9824902-A1
                                                                                                                                                                                                                                                                  11-JUN-1998
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developmental biology; cell signalling; insecticide;

Drosophila melanogaster.

pharmaceutical

Drosophila;

WO200171042-A2

27-SEP-2001

Myers EW;

Li PWD,

Adams M,

Venter JC,

(PEKE) PE.CORP NY

23-MAR-2001; 2001WO-US009231. 23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150.

Drosophila melanogaster polypeptide SEQ ID NO 31152.

26-MAR-2002 (first entry)

(first entry

02-JUL-1999

AAY07018

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The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HIA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated cancer associated nucleic acids and polypeptides - isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers.
                                                                                 associated antigen; diagnosis; research; treatment; human; cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DTVPDNHRNKFKVINVDDDGNELGSGIMELTDTELILYTRKRDSVKWHYLCLRRYGYDSN
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                                                       Breast cancer associated antigen precursor sequence.
                                                                                                                                                                                                                                                                                                                                                                                         Chen 3
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Pred. No. 5.9e-39;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                          Stockert E, Gure A, C
Pfreundschuh M, Tureci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 398; 787pp; English
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97US-0061599P.
97US-0061765P.
97US-00948705.
97GB-00021697.
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98.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          Scanlan MJ,
Obata Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-132448/11
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es 72; Conserv
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                                                                                                                prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                (LUDW-) LUDWIG
                                                                                                                                                                                                                                                         17-JUL-1997;
10-OCT-1997;
10-OCT-1997;
10-OCT-1997;
11-OCT-1997;
22-JUN-1998;
                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                15-JUL-1998;
                                                                                                                                                                                                     28-JAN-1999
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                                                                                    Cancer
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Matches
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ABB68120
ID ABB6
XX
AC ABB6
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Y, Gout Sahin U;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 SFEAGRECMSGPGIYTFRVHNAEQLYPMFQRXINAVNTDAFVQGERERVNSAHSVSVNMG 135
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1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 HRNKFKV----INVDDDGNELGSGIMELIDTELILYTRKRDSVKWHYLCLRRYGYDSNLF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL10511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS737-ABB72072). The sequence data for this parent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 31152; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25.0%; Score 174; DB 4; Length 442; 34.4%; Pred. No. 7.6e-12; tive 22; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            p62 protein downstream of tyrosine kinases (p62-dok).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p62-dok; protein downstream of tyrosine kinases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW62507 standard; protein; 481 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABL12223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 442 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RT 122
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                                                                                                                                                                                                                                                                                                                                                                                                               interactions.
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o; 9 83

Gaps ·,

1; Indels

ABB68120 standard; protein; 442 AA.

ABB68120,

Length 101;

New polynucleotides and polypeptides for predicting the activity of compounds that interact with protein tyrosine kinases and/or protein

Lee FY, ႘

Fairchild CR,

Huang F,

WPI; 2003-636735/60. N-PSDB; ADD14695.

17-JAN-2003; 2003WO-US001981, 18-JAN-2002; 2002US-0350061P. (BRIM) BRISTOL-MYERS SQUIBE

WO2003062395-A2 Homo sapiens.

31-JUL-2003

Claim 10; SEQ ID NO 288; 139pp; English

compounds that interact w

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The present sequence represents p62-dok (protein downstream of tyrosine mammasian cells after stimulation with a ligand for a receptor tyrosine kinase found in oncogenic cells. The p62-dok protein binds p120 ras GTPase-activating protein (GAP). The p62-dok protein binds p120 ras GTPase-activating protein (GAP). The p62-dok protein is involved in a signal transduction pathway initiated by receptor tyrosine kinase, and is rapidly tyrosine phosphorylated. The p62-dok protein is also present in normal cells, but is not constitutevely phosphorylated by normal receptor tyrosine kinase. Antibodies against p62-dok and aberrantly phosphorylated 62-dok, and probes derived from the p62-dok mase event in the diagnosis and treatment of conditions in which an oncogenic tyrosine kinase is active such as chronic myelogenous leukaemia (CML) and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Newly isolated human p62-dok protein - used to develop products for the diagnosis and treatment of conditions in which oncogenic tyrosine kinase is active, e.g. chronic myelogenous leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 GSGIMELTDTELILYTRKRDS-----VKWHYLCLRRYGYDSNLFSFESGRRCQTGQGIF 77
tyrosine phosphorylation; receptor tyrosine kinase; oncogenic cell; pl20 ras GTPase-activating protein; GAP; signal transduction pathway; antibody; diagnosis; treatment; chronic myelogenous leukaemia; CML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           predictor set; protein tyrosine kinase activity modulator; protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic; gene therapy; drug sensitivity; genetic profile; cancer; human.
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                                                                                                                                                                                                                                                                                                                                      Clarkson BD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 AFKCARAEELFINMLQEIMQNNSINVVE---EPVVERNNHQTELEVPRTPRTP 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.6%; Score 143.5; DB 2; Length 4
29.5%; Pred. No. 4.1e-08;
.ive 20; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                      Strife AO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human src biomarker polypeptide SEQ ID NO:288.
                                                                                                                                                                                                                                                                                                                                    Carpino NA, Kobayashi R, Wisniewski DG,
                                                                                                                                                                                                                                                                                COLD SPRING HARBOR LAB.
SLOAN KETTERING INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADD14099 standard; protein; 509 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 2A-C; 86pp; English.
                                                                                                                                                                                            97WO-US019788.
                                                                                                                                                                                                                           96US-0030418P.
97US-00787091.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAV38415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 481 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human cancers
                                                      human cancer
                                                                                                                     WO9820129-A1
                                                                                                                                                                                            30-OCT-1997;
                                                                                                                                                                                                                           01-NOV-1996;
22-JAN-1997;
                                                                                                                                                        14-MAY-1998.
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                                                                                     Mammalia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADD14099;
                                                                                                                                                                                                                                                                                (COLD-) (SLOK ) 8
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The present invention describes a predictor set comprising a plurality of polymucleotides or polypeptides whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein tyrosine kinase activity or members of the protein tyrosine kinase activity or members of the protein tyrosine kinase to pathway. Also described: (1) predicting whether a compound is capable of conformating whether the cells, comprising obtaining a sample of cells, correlating whether the cells express a plurality of markers, and correlating the expression of the markers to the compound's ability to correlate with compound sensitivity or resistance of cells associated with a disease state, and (3) identifying polymucleotides and collypeptides whose expression levels correlate with compound sensitivity or resistance of cells associated with a disease state, comprising subjecting the plurality of associated with a disease state, comprising subjecting the plurality of an increarray of polymucleotides or polypeptides, and selecting compounds, analysing the expression pattern of a microarray of polymucleotides that predict the sensitivity or resistance of cells associated with a disease state by using the expression pattern of cells associated with a disease state by using the expression pattern of cells associated with a disease state by using the expression pattern of the microarray. The polymucleotides and cells expression pattern of the microarray of polymorphical with a disease state by using the expression pattern of the microarray. The polymucleotides and cells associated with a disease state by using the expression pattern of the microarray. The polymorphical subjection is an even or more companions, and selecting the prediction of cells associated with a disease state by using the expression pattern of the microarray. The polymorphical subjections and conformations and conformations and conformations and conformations and conformations.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The polynucleotides and polypeptides are useful in predicting the activity of compounds that interact with protein tyrosine kinases and/or protein tyrosine kinases and/or sensitivity in patients to allow the development of individualized sensitivity in patients to allow the development of individualized cancer; based on patient response at a molecular level. The present sequence is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.6%; Score 143.5; DB 7;
29.5%; Pred. No. 4.4e-08;
ive 20; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG66871 standard; protein; 541 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Best Local Similarity
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New prostate specific polypeptides useful for identifying, diagnosing, monitoring, staging, imaging and treating prostate cancer and non-
                                                      prostate specific protein; cytostatic; PSP; prostate cancer;
                                                                                 gene therapy; vaccine; non-cancerous prostatic disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sun Y, Liu
Human prostate specific protein DEX0283_179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 230-233; 248pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancerous disease states in prostate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recipon H,
                                                                                                                                                                                                                                                                                                            20-NOV-2001; 2001WO-US045177.
                                                                                                                                                                                                                                                                                                                                                                        21-NOV-2000; 2000US-0252189P.
                                                                                                                                                                                                                                                                                                                                                                                                                              (DIAD-) DIADEXUS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-500278/53.
                                                                                                                                                                                                WO200242329-A2.
                                                                                                                                                                                                                                                         30-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salceda S,
                                                            Human;
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The invention relates to an isolated polypeptide that comprises a sequence with 60 % sequence identity to one of 103 prostate specific cepted by a nucleic acid comprising one of 114 prostate specific mucleic concoded by a nucleic acid comprising one of 114 prostate specific mucleic acid (PSNA) sequences (S2), given in specification. Also included are a vector comprising the PSNA, a host cell comprising the vector, and the PSNA, a host cell comprising the vector of the PSNA, a host cell comprising the vector of the PSNA, a host cell comprising the vector of the PSNA, and a vector comprising the presence of cancer in a patient, comprising a unit for and a vaccine comprising the PSP or the PSNA, in a sample of a patient and a vaccine comprising the PSP is useful for determining the presence of a prostate specific nucleic acid (PSNA) in a sample. The antibody to the PSP is useful for determining the prostate cancer, where the administration of the antibody induces an immune response against the prostate cancer cell carting a patient with prostate cancer, where the administration of the antibody induces an immune response against the prostate cancer cell carting the nucleic acid molecule or polypeptide. The PSPP or the PSNA is useful for dagnosing and monitoring the presence and metastases of prostate cancer in a patient. The PSN is useful for identifying an agonist and antagonist. The PSNA is useful for detecting prostate cancer by detecting genetic lesions or mutations. The PSP and the PSNA are useful for detecting genetic lesions or mutations. The PSP and the PSNA are useful for detecting genetic lesions or mutations. The PSP and the PSNA are useful for detecting genetic lesions or mutations. The PSP the PSPA the cancer where the pSPA and the PSNA are useful for detecting genetic lesions or mutations. The PSP the PSPA the PSNA and the antibody are useful for identifying prostate cancer. The PSP and the PSNA are useful for detecting genetic lesions or mutations. The PSP the PSPA the pSNA and the antibody are usefu diagnosing, monitoring, staging, imaging and treating prostate cancer and non-cancerous disease states in prostate tissue. The present sequence is a prostate specific protein (PSP) sequence

77 24 GSGIMELTDTELILYTRKRDS-----VKWHYLCLRRYGYDSNLFSFESGRRCQTGQGIF 9; Gaps Length 541; Indels 20.6%; Score 143.5; DB 5; 29.5%; Pred. No. 4.8e-08; ative 20; Mismatches 50; Query Match 20.64 Best Local Similarity 29.54 Matches 33; Conservative Sequence 541 AA;

78 AFKCARAEELFNMLQEIMQNNSINVVE---EPVVERNNHQTELEVPRTPRTP 126

248 ĠSYVLRVEAERLTLIVGAQSQILEPLISWPYTLLRRYGRDKVMFSFEAGRRCPSGFGTF 307

В

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The present sequence is that of a mouse haematopoietic stem cell (HSC) specific protein. It is an example of claimed HSC specific proteins (see AAY29176-93) predicted from movel isolated HSC specific nucleic acids (see AAZ94077-111). The HSCS are especially primitive HSCS (PHSCS) such as umbilical cord cells, bone marrow cells and foetal liver cells. The encoded proteins are growth factors, transcription factors, splicing factors, transport proteins, translation factors or replication factors. The invention provides claimed methods: CC differentiation or replication. The invention provides claimed methods: CC in a sample in for identifying PHSC specific nucleic acids, for generating a stem coll/progenitor cell from PHSCs; for identifying the presence of a PHSC in a sample in for identifying the presence in a sample of a compound that modulates HSC activity; for using such a compound to treat an immune system condition, especially leukaemia; for introducing exogenous nucleic acidinto a HSC; and for ex vivo expansion of HSCs Also claimed are vectors, host cells, and an antibody that specifically binds a an HSC-specific protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --EPVVERNNHOTELEVPRTPR 124
                                                                                                                                                                                                                                                                                                                                                             /note= "nucleotide sequence encoding this protein has an in-frame stop codon following Leu codon 343"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGSGIMELTDTELILYTRKRDSVKWHYLCLRRYGYDSNLFSFESGRRCOTGOGIFAFKCA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hematopoietic stem cell signaling proteins modulating replication and differentiation for treating immune system disorders and leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 24; Gaps
308 TFQTAQGNDIFQAVETAIHRQKAQGKAGQGHDVLRADSHEGEVAEGKLPSPP 359
                                                                                                                                                                                                                                   stem cell; immune system disorder; leukaemia; immunomodulator; therapy; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.3%; Score 141; DB 3; Length 359; 28.3%; Pred. No. 5.5e-08; ive 20; Mismatches 47; Indels
                                                                                                                                                                                                    Haematopoietic stem cell specific protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 21; Page 232-233; 256pp; English
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                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                              Ź
                                                                                              AAY79184 standard; protein; 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US019052.
                                                                                                                                                                 (first entry)
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Best Local Similarity 28.3%
Matches 36; Conservative
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N-PSDB; AAZ94125.
                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                         Haematopoietic
antileukaemic;
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                                                                                                                               AAY79184;
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anorectic; gene therapy; vaccine; cancer; neurodegenerative disorder;
Parkinson's disease; metabolic disorder; diabetes; obesity;
RAPDICGVVAAAIARQRERLPELAMSPPCPLPRALSLPSLEPPGELREVAPGFELPTPRK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACF06233 to ACF06242 encode the human NOVX proteins given in ABR83334 to ABR83343, designated NOVIa, NOV2a, NOV3a, NOV4a, NOV4b, NOV5a, NOV6a, NOV7a, NOV6Ba and NOV9a respectively. NOVX sequences can have cytostatic, antidiabetic, neuroprotective, antiparkinsonian and anorectic activities, and can be used in vaccines and gene therapy. The NOVX polypeptides can be used for preparing a composition for treating or preventing a pathology associated with the NOVX-polypeptides e.g. cancer, neurodegenerative disorders such as Parkinson's disease, or metabolic disorders such as diabetes or obesity, or for tissue typing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New NOVX polypeptide, useful for preparing a composition for treating or preventing e.g. cancer, neurodegenerative disorders such as Parkinson's disease in metabolic disorders such as diabetes or obesity, or for tissue typing.
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L, Patturajan M;
EZ, Zhong M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DW, Boldog FL, Burgess CE, Catt.
Guo X, Ji W, Kekuda R, Li L, P.
Spytek KA, Vernet CAM, Voss EZ,
                                                                                                                                                                                                                                                                      ABR83336 standard; protein; 331 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human NOV3a protein SEQ ID NO:6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-MAY-2002; 2002US-0381495P-
28-MAY-2002; 2002US-038344P-
29-MAY-2002; 2002US-0384024P-
07-AUG-2002; 2002US-0401788P-
31-OCT-2002; 2002US-0406153P-
31-OCT-2002; 2002US-0405756P-
02-DEC-2002; 2002US-0422756P-
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20-DEC-2001, 2001US-0342592P.
31-DEC-2001, 2001US-0342693P.
17-AFR-2002, 2002US-0373288P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-DEC-2002; 2002WO-US038821
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Shenoy SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP.
                                                            TP-TTPG 130
                                                                                                                        LPLTDPG 305
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N-PSDB; ACF06235.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tissue typing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-DEC-2001;
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                                                                                                                        299
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                                                            125
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Score 137.5; DB 6; Length 331;

19.8%;

Query Match

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                                                                                        153 GECTMQITHENIYLWDIHNAKVKLVMWPLSSLRRYGRDSTWFTFESGRMCDTGEGLFTFQ 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang D;
Zhao QA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
                                                          24 GSGIMELIDTELILYTRKRDSVK---WHYLCLRRYGYDSNLFSFESGRRCOTGQGIFAFK
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                          peripheral nervous system; neuropathy; central nervous system; CNS; Alzhener's; Parkinson's disease; hauntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ren F, Wa
Zhang J,
                            13;
                                                                                                                                           213 TREGE----MIYQKVHSATLAIAEQHERLMLEMEEQKARLQTSLTEPMT 256
                                                                                                                      81 CARAEELFNMLQEIMQNNSINVVEE-----PVVERNNHQTELEVPRT
                          42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qian XB,
Yang Y,
           Pred. No. 1.3e-07;
; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ma Y, C
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; SEQ ID NO 2951; 10078pp; English.
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nrman T, Xu C, X
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                             immunosuppressant;
                                                                                                                                                                                                                                  AAM39806 standard; protein; 337 AA
                                                                                                                                                                                                                                                                                                                            Human polypeptide SEQ ID NO 2951.
31.5%; ***. 19; **
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2000US-00552317
2000US-00598042
2000US-0059815
2000US-00653450
2000US-00653450
2000US-00653450
2000US-0062191
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Wang Z, Wehrman T,
Goodrich R, Drmanac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000WO-US034263
                                                                                                                                                                                                                                                                                              (first entry)
                             Conservative
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           Local Similarity
les 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                             Human; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAI58962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200153312-A1.
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14-SEP-2000;
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25-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         leukaemia
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Wang J,
Zhou P,
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                                                                                                                                                                  GECTMQITHENIYLWDIHNAKVKLVWMPLSSLRRYGRDSTWFTFESGRMCDTGEGLFTFQ 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang D;
, Zhao QA;
                                                                                                                                                 GSGIMELTDTELILYTRKRDSVK---WHYLCLRRYGYDSNLFSFESGRRCQTGQGIFAFK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; gene therapy; cancer;
assays for receptor activity, arthritis and inflammation, leukaemias of C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, nootropic, immunosuppressant, cytostatic, gene therapy, cancer peripheral nervous system; neuropathy, central nervous system; CNS; Alzheimer's, Parkinson's disease; Huntington's disease; haemostatic, amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic, chemokinetic, thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nel nucleic acids and polypeptides, useful for treating disorders central nervous system injuries.
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Zhang J,
                                                                                                                      13;
                                                                                                                                                                                                            81 CARAEELFUMLOEIMQNNSINVVEE-----PVVERNNHQTELEVPRT 122
                                                                                          Length 337;
                                                                                                                                                                                                                           TREGE----MIYOKVHSATLAIAEQHERLMLEMEQKARLQISLTEPMT
                                                                                                                      Indels
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Yang Y,
                                                                                        19.8%; Score 137.5; DB 4; 31.5%; Pred. No. 1.3e-07; ive 19; Mismatches 42;
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Α.Τ,
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irman T, Xu C, )
Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                      Human polypeptide SEQ ID NO 6523.
                                                                                                                                                                                                                                                                                                                 AAM41592 standard; protein; 365
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21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
20-JUL-2000; 2000US-00598042.
19-JUL-2000; 2000US-00653450.
14-SEP-2000; 2000US-00653450.
14-SEP-2000; 2000US-00693036.
29-NOV-2000; 2000US-00593036.
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Wang Z, Wehrman T,
Goodrich R, Drmanac
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                                                                                                                        Conservative
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N-PSDB; AAI60748.
                                                                                       Query Match
Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                               Sequence 337 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200153312-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                         22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leukaemia
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Wang J, I
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                                                                                                                                                                                                                                                                                                                                               AAM41592;
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                                                                                                                                                                                                                                                                                  RESULT 13
AAM41592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80
system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic as througholytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
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, Zhao Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 GSGIMELTDTELILYTRKRDSVK---WHYLCLRRYGYDSNLFSFESGRRCQTGQGIFAFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, nootropic, immunosuppressant, cytostatic, gene therapy, cancer peripheral nervous system, neuropathy, central nervous system, CNS, Alzheimer's, Parkinson's disease; Huntington's disease; haemostatic, amyotrophic lateral sclerosis, Shy-Drager Syndrome, chemotactic, chemokinetic, thrombolytic, drug screening, arthritis; inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                          13; Gaps
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                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARAEELFNMLQEIMQNNSINVVEE-----PVVERNNHQTELEVPRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 TREGE----MIYQKVHSATLAIAEQHERLMLEMEQKARLQTSLTEPMT
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                        19.8%; Score 137.5; DB 4; 31.5%; Pred. No. 1.5e-07; iive 19; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ma Y,
Xue AJ,
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irman T, Xu C, )
Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-00471275.
2000US-00488725.
200US-00552317.
200US-00598042.
2000US-00620312.
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2000US-00693036.
2000US-00727344.
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Wang Z, Wehrman T,
Goodrich R, Drmanac
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                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 31.5%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-442253/47.
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                                                                                                                                                                                                                                                                                                                  Sequence 365 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-DEC-1999;
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Wang J,
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymuclectides are useful in gene therapy. A composition containing a polypeptide or polymuclectide of the invention may be used to treat diseases of the peripheral nervous sipturies, peripheral nervous injuries, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic cateriosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolyty cateriotity, cancer diagnosis and therapy, drug screening, assays for receptor activity, ancer diagnosis and inflammation, leukaemias and CNNS disorders. Note: The sequence data for this patent did not form part of the printed specification
Example 2; SEQ ID NO 6524; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 365 AA;
8 X 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 X 8
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181 GECTMQITHENIYLWDIHNAKVKLVMWPLSSLRRYGRDSTWFTFESGRMCDIGEGLFTFQ 240 24 GSGIMELIDIELILYTRKRDSVK---WHYLCLRRYGYDSNLFSFESGRRCQTGQGIFAFK 80 13; DB 4; Length 365; TREGE----MIYOXVHSATLAIAEQHERLMLEMEQXARLOTSLITEPMT 284 81 CARAEELFNMLQEIMQNNSINVVEE-----PVVERNNHQTELEVPRT Indels 19.8%; Score 137.5; DB 4; 31.5%; Pred. No. 1.5e-07; tive 19; Mismatches 42; Conservative Query Match Best Local Similarity Пр ò 셤

AAB52062 standard; protein; 412 AA

AAB52062;

(first entry) 21-FEB-2001

Gene 2 human secreted protein homologous amino acid sequence #111.

2, 2004, 09:29:30

Search completed: August

Job time : 84.1053 secs

Human, secreted protein, cytostatic, immunosuppressive, nootropic, neuroprotective, antiviral; antiallergic, hepatotropic, antidiabetic; antillerglammatory; antiluleer; vullnerary; anticonvulsant; antibacrerial; antifungal, antiparasitic, cardiant, cancer; immune disease; allergy; cardiovascular disorder; wound healing; infection; neurological disease.

Homo sapiens

WO200061596-A1

19-OCT-2000.

HOLD SEA A CAN A C

06-APR-2000; 2000WO-US008983

14-JAN-2000; 2000US-0176068P 09-APR-1999;

HUMA-) HUMAN GENOME SCI INC ROSEN C A. (ROSE/)

Komatsoulis Ruben SM,

ö

WPI; 2000-611865/58.

Fifty nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases.

Disclosure; Page 11; 505pp; English

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CC human secreted proteins AABS2012 - AABS2161. Sequences AABS2062 - AABS2103 represent alternative polypeptides encoded by the genes, and amino acid sequences with which they share homology. The genes and proteins have activities dependent on the tissues and cells in which they care expressed. Examples of their activities include cytostatic; are expressed. Examples of their activities include cytostatic; aminousuppressive, nootropic, neuroprotective, antiviral, antiallargic; hepatotropic; antidabetic; antiinflammatory; antiviral, antiallargic; anticonvulsant; antibacterial; antiinflammatory; antiviral; and cardiant. The secreted proteins, polypeptides, antagonists and agonists may be anticonvulsant; antibacterial; antifundary diseases and disorders cuseful in treating, preventing and/or diagnosing diseases and disorders such as cancer; particularly breast and ovariant cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, lung, or urogenital. Immune disorders such as Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, cardiovascular disorders such as myocardial ischaemias; wound healing; neurological diseases such as myocardial ischaemias; wound healing; neurological diseases such as creebral anoxia and epilepsy; and infections may also be treated using the proteins and polynucleotides of the invention. Sequences AAC95512 - AAC95520 and AABS2011 are used in the isolation and characterisation of the proteins and polynucleotides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 WHYLCLRRYGYDSNLFSFESGRRCQTGQGIFAFKCARAEELFNMLQEIM--QNNSINVVE 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 412;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |----OPATIPASLPRPDSPYSRPHDSLPPPSPTTP 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.4%; Score 135; DB 3; 34.0%; Pred. No. 3.5e-07; ive 13; Mismatches 33
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August 2, 2004, 09:26:54; Search time 19:6711 Seconds (without alignments) 635.701 Million cell updates/sec
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1 DIVPDNHRNKFKVINVDDDG......NNHQTELEVPRTPRTPG 130
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                   283366 seqs, 96191526 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1: pir1:*
2: pir2:*
3: pir3:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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				m	10	-		61			-	m	•		m	0.1	•	•	-	10	~	-			10	-44	•	_	
5	ID	T32819	T08731	S16948	830185	JS0670	T48191	T00352	C96668	139171	A47550	T37308	T04499	D70313	T37958	T30562	BVBYD9	D71608	H72360	S77476	C90073	JC5209	F86196	WIMIE	T06636	T23064	F87908	T43291	
	DB	2	7	Н	~	~	~	~	N	N	~	N	7	N	~1	N	Н	Ŋ	N	N	7	N	~1	-	(7	N	~	0	•
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* Ouery	Match	25.6	17.9	11.8	11.2	11.2	10.8	10.8	10.8	10.8	10.5	10.4	10.3	10.3	10.3	10.3	10.3	10.2	10.1	10.1	10.1	10.1	10.0	10.0	10.0	10.0	10.0	10.0	•
	Score	178	124.5		78	78	75.5	75.5	75.5	75	73	72.5	72	72	72	72	71.5	71	70.5	70	70	70	69.5	69.5	69.5	69.5	69.5	69.5	()
Result	No.	ч	7	m	4	ιΩ	φ	7	80	σ	10	11	. 12	13	14	15	16	17	18	19	20	21	22	23	. 24	25	26	27	c

ETS domain protein hypothetical prote DNA helicase/prima 88K E-26-specific hypothetical prote glutathione-regula surface antigen sp surface antigen pa GTP-binding protein unknown protein F2 Mutator-like trans hypothetical prote histidine kinase hypothetical prote DNA-directed RNA p	elegans 999 #text_change 29-Oct-1999 97 d F54D12.	A;Cross-references: EMBL:AF040647; PIDN:AAB94991.1; GSPDB:GN00020; CESP:F54D12.6 B;Experimental source: strain Bristol N2; clone F54D12 C;Genetics: A;Gene: CESP:F54D12.6 A;Map postition: CESP:F54D12.6 A;Thtrons: G3/1:117/3
743315 745843 745843 745843 746193 746193 806839 806839 806839 8064729 819429 719480 719486 7121386	RESULT 1 T32819 Mypothetical protein F54D12.6 - Caenorhabditis eleg C, Date: 29-0ct-1999 #sequence_revision 29-0ct-1999 C, Accession: T32819 R, Maggi, L.; Goela, D. Submitted to the EMBL Data Library, December 1997 A, Description: The sequence of C. elegans cosmid F5A, Accession: T32819 A, Accession: T32819 A, Status: preliminary; translated from GB/EMBL/DDBJA, Rescule type: DMA A, Residues: 1-195 cMAG>	47; PIDN:AAB94991 ristol N2; clone
0 0 1 1 0 0 0 1 1 0 0 0 1 1 0 0 0 1 1 0 0 0 1 0	.6 - legar ce_re cibra of C	0406 in B
2447 1200 1200 1200 1200 1200 1200 1200 120	protein F54D12.6 tenorhabditis elegenti-12819 #sequence Goela, D. the EMBL Data Lik the EMBL Data Lik The sequence of unmber: 221228 T32819 tilminary; transians of the Fee Company transians the sequence of the Fee Company transians transians the Fee Co	MBL:AF
	protein F enorhabdi tt-1999 # T32819 # GGolan D. the EMBL D. the EMBL D. The Seq T1000 # T100	erences: EM tal source: P:F54D12.6 ion: 2
\$	RESULT 1 132819 hypothetical protein F54D12.6 - Ca C.Species: Caenorhabditis elegans C.Date: 29-Oct-1999 #sequence_revi C.Accession: T32819 R.Maggi, L., Goela, D. Submitted to the EMBL Data Library A.Description: The sequence of C. A.Accession: T32819 A.Status: preliminary; translated A.Status: preliminary; translated A.Residues: 1-195 kMG>	A) Cross references: A, Experimental sour C, Genetics: A, Gene. CESP: F54D12 A, Map position:
0	RESULT 1 132819 hypothetical hypothetical C;Date: 29-0c C;Accession: R;Maggi, L.; R;Maggi, L.; A;Description A;Description A;Accession: A;Accession: A;Status: pre A;Rolecule ty A;Residues: I	A) Cross-red A) Experimen C) Genetics A) Gene: CES

ζ	7 HRNKFKVINVDDDGNELGSGIMELTDTELLLYTRKRDSVKWHYLCLRRYGYDS-NLFSFE 65
Db 42	
. 92	66 SGRRCQTGQGIFAFKCARAEELFNMLQEIMQNNSINVVEEPVVERN-NHQTELEVPRTPR 124
Db da	94 SGRRCESGEGGMFTFQSKKADEIFQLIQSLIEEFANTSMEKQNMENSFRYQRQQSVPISSR 153
RESULT 2	
T08731	
hypothetical	hypothetical protein DKFZp566A0946.1 - human (fragment)
C;Species: Ho	C; Species: Homo sapiens (man)
C;Date: 11-Ju	C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C;Accession: T08731	T08731
R;Ottenwaeld6	R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to	submitted to the Protein Sequence Database, May 1999
A;Reference r	A;Reference number: Z16474
A; Accession: T08731	108731
A; Molecule type: mRNA	pe: mRNA
A;Residues: 1-265 <ott></ott>	-265 <ott></ott>
A;Cross-refer	A;Cross-references: EMBL:AL050069
A; Experiments	A; Experimental source: fetal kidney; clone DKFZp566A0946
C;Genetics:	
A; Note: DKFZp566A0946.1	566A0946.1

17.9%; Score 124.5; DB 2; Length 265;

Query Match

ж ;

Gaps

Query Match 25.6%; Score 178; DB 2; Length 195; Best Local Similarity 32.5%; Pred. No. 2.7e-11; Matches 39; Conservative 30; Mismatches 41; Indels 10;

ij

Gaps

243

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A,Molecule type: protein appears to be the major substrate for insulin-stimulated tyrosine C,Comment: This protein appears to be the major substrate for insulin-stimulated tyrosine o dock various proteins containing the phosphotyrosine-binding Src-homology domain 2 (SH. C,Comment: This protein contains at least 11 PEST regions, which suggests rapid turnover.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A map position: 2436-2436
A fintrons: #status absent
C;Superfamily: insulin receptor substrate IRS-1; pleckstrin repeat homology
C;Keywords: ATP; phosphoprotein
C;Keywords: ATP; pleckstrin repeat homology <PLK>
F)1-113-100main: pleckstrin repeat homology <PLK>
F;46-465,551,612,622,662,732,941,989,1012/Binding site: phosphate (Tyr) (covalent) #statu
F;78,527,1100,1223/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #s
F;161/Binding site: ATP predicted
F;189,323,441,624,536,795,920,984,1084,1218/Binding site: phosphate (Ser) (covalent) (by
F;300,351,774/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status prec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 23-Aug-1996 #text_change 16-Jul-1999
C;Accession: I53160; JS0670; PN0678
C;Accession: I53160; JS0670; PN0678
B;Azaki, B.; Sun, X.J.; Haag, B.L.; Chuang, L.; Zhang, Y.; Yang-Feng, T.L.; White, M.; Kabiabetes, 42, 1041-1054, 1993
A;Title: Human skeletal muscle insulin receptor substrate-1. Characterization of the CDN;
A;Reference number: I53160; MUID:93292738; PMID:8513971
A;Title: Cloning of the mouse insulin receptor substrate-1 (IRS-1) gene and complete sequesterence number: S43514, MJID:94220494; PMID:8167159
A;Accession: S43514
A;Accession: S43514
A;Residues: preliminary
A;Molecule type: mRNA
A;Residues: 1-1037, AS, 1038-1179, 'H',1181-1231 cARA>
A;Residues: 1-1037, AS, 1038-1179, 'H',1181-1231 cARA>
A;Cross-references: EMBL:L24563; NID:9407993; PIDN:AAAA9335.1; PID:9407994
C;Superfamily: insulin receptor substrate IRS-1; pleckstrin repeat homology
F;11-113/Domain: pleckstrin repeat homology cPLK>
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Ajaccession: 153160
Ajaccession: Standated from GB/BMBL/DDBJ
Ajaccession: trandated from GB/BMBL/DDBJ
Ajaccession: Standated from GB/BMBL/DDBJ
Ajaccession: 1-1242 <RES
Ajaccession: 1-1242 <RES
Ajaccession: 1-1242 <RES
Ajaccession: USB SSESSION: 183, 280-285, 1992
Bjochem. Bjophys. Res. Commun. 183, 280-285, 1992
Ajaccession: USB SSESSION: WUID:92181456; PMID:1311924
Ajaccession: USB SSESSION: USB SSESSION: USB STANDER SSESSION: USB SSESSION
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A,Residues: 1-134, 'G',135-361, 'R',363-383,'R',385-1242 <NIS>
A,Residues: 1-134, 'G',135-361, 'R',363-383,'R',385-1242 <NIS>
A,Crose-references: GB.S85963; NID:9246465; PIDN:AAB21608.1; PID:9246466
A,Experimental source: hepatocellular carinoma cell line FOCUS
R,Smith, D.K.; Bradshaw, M.; Croall, D.E.; Garner, C.W.
Biochem. Biophys. Res. Commun. 196, 767-772, 1993
A,Title: The insulin receptor substrate (IRS-1) is a PEST protein that is susceptible than the substrate (IRS-1) is a PEST protein that is susceptible than the substrate (IRS-1) is a PEST protein that is susceptible than the substrate (IRS-1) is a PEST protein that is susceptible than the substrate (IRS-1) is a PEST protein that is susceptible than the substrate (IRS-1) is a PEST protein that is susceptible than the substrate (IRS-1) is a PEST protein that is susceptible than the substrate (IRS-1) is a PEST protein that is susceptible than the substrate (IRS-1) is a PEST protein that is susceptible than the substrate (IRS-1) is a PEST protein that is susceptible than the substrate (IRS-1) is a PEST protein that is susceptible than the substrate (IRS-1) is a PEST protein that is susceptible than the substrate (IRS-1) is a PEST protein that is susceptible than the substrate (IRS-1) is a PEST protein that is susceptible than the substrate (IRS-1) is a PEST protein that is susceptible than the substrate (IRS-1) is a PEST protein that is susceptible than the substrate (IRS-1) is a PEST protein that is susceptible than the substrate (IRS-1) is a PEST protein than the substrate (IRS-1) is a PES
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10;
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Pred. No. 10;
7; Mismatches 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 78;
Pred. No.
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Best Local Similarity 30.0
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 NHQTELEVPR
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Best Local Similarity
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A; Mesidues: 1-1235 <SUNA
A; Mesidues: 1-1235 <SUNA
A; Cross-references: BMBL:X58375; NID:956503; PIDN:CAA41264.1; PID:956504
R; Rothenberg, P.L.; Lane, W.S.; Karasik, A.; Backer, J.; White, M.; Kahn, C.R.
R; Rothenberg, P.L.; Lane, W.S.; Karasik, A.; Backer, J.; White, M.; Kahn, C.R.
A; Biol. Chem. 266, 8302-8311, 1991
A; Rile: Purification and partial sequence analysis of pp185, the major cellular substra
A; Reference number: A39811; MUID:91217066; PMID:2022647
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A; Molecule type: protein
A; Mesidues: 44-51;173-178;223-243;489-506;635-646;871-882,'I',884,'X',886-888;932-936,'X
A; Note: the phosphotyrosine residue was not identified
C; Comment: This protein and the beta chain of the insulin receptor itself are the major
C; Comment: Phosphorylation of this protein in response to insulin is maximal at 30 secon
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C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
C;Accession: S30.185; S45.31
B;Keller, S.R.; Aebersold, R.; Garner, C.W.; Lienhard, G.E.
Biochim. Biophys Acta 1172, 323-326, 1993
A;Title: The insulin-elicited 160 kDa phosphotyrosine protein in mouse adipc A;Reference number: S30185; MUID:93192326; PMID:8448209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
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A,Residues: 1-1231 <KEL>
A,Cross-references: EMBL:X69722; NID:g297913; PIDN:CAA49378.1; PID:g297914
R,Araki, E.; Haag III, B.L.; Kahn, C.R.
Biochim. Biophys. Acta 1221, 353-356, 1994
                                                                                                                                                                                              GSGIMELTDTELILYTRKRDSVK---WHYLCLRRYGYDSNLFSFESGRRCQTGQGIFAFK
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                                                                                         Indels
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                                                                                         Mismatches
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                                       Pred.
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Matches 24, Conservative
                                                                                         Conservative
                                       Best Local Similarity
Matches 30; Conser
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UKNOWN protein F15H21.18 [imported] - Arabidopsis thaliana Gispecies: Arabidopsis thaliana (mouse-ear cress)
Gispecies: Arabidopsis thaliana (mouse-ear cress)
Cidacession: C9666
RiTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Anshor, N.F.; Hudres, B.; Hulzar, L.
Nature 408, 1816-80, 2000
G.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Martin, E.; Kim, C.C., A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Martin, E.; Kim, C.C., A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.Hinn, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.Fitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.Raccession: C96668
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              -GRRCQTGQGIFAFKCARAEELFNMLQEIMQNNSINV 102
                                                     179 YREDSNILSFDSDGNQNILSSTLTSKGNETIESIF----KAEDLLPEAASLSENLDISK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 MLFSFTSIGGKVDHCLPKGR----GPNMFAIQGALKPKSVAKAKFQQLYIVDTENEVNNR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GB: AE005173; NID: g10645404; PIDN: AAG21522.1; GSPDB: GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 NLFSFES------GRRCQTGQGIFAFK------CARAEELFNMLQEIMQNNS 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cyclin A/CDK2-associated p45 - human
C;Species: Homo sapiens (man)
C;Date: 23-Reb-1996 #sequence_revision 23-Reb-1996 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CyAccesion: 139171
Rizhang, H.; Kobayashi, R.; Galaktionov, K.; Beach, D.
Cell 82, 915-925, 1995
A;Title: pi98kpl and p458kp2 are essential elements of the cyclin A-CDK2 S
A;Title: pi98kpl and p458kp2 are essential elements of the cyclin A-CDK2 S
A;Accession: 139171
A;Status: preliminary
A;Molecule type: mRNA
A;Coss-treferences: EMBL:U33761; NID:g995825; PIDN:AAC50242.1; PID:g995826
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 NHRNK-----FKVINVDDDGNELGSGIMELTDTELILYTRKRDSVKWHYL-CLRRYGYDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
10.8%; Score 75.5; DB 2; Length 7
Best Local Similarity 24.4%; Pred. No. 10;
Matches 33; Conservative 26; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
5.7;
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Pred. No.
                                                                                                              103 VEEPVVERNNHQTELEVPRTPRTP 126
                                                                                                                                                                      234 EETPPVRTLKSQSSLSGKPKERCP 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 INVVEEPVVERNNHQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 YNIMRLRYIKNNQPQ 154
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C;Keywords: cell cycle control
           55 YGYDSNLFSFES
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA A;Residues: 1-753 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Gene: F15H21.18
A,Map position: 1
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(Species: Homo sapiens (man)
(Species: Homo sapiens (man)
(Species: Ol-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
(SAccession: T00352
(Rishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.
DNA Res: S, 169-176, 1998
A;Title: Frediction of the coding sequences of unidentified human genes. X. The complete
A;Reference number: 214142; MUID:98403880; PMID:9734811
                                                                                                                                                                                                                                                                                        RESULT 6
Hydrothetical protein F7A7.220 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear oress)
C;Species: Arabidopsis thaliana (mouse-ear oress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 28-Jul-2000
C;Accession: T48391
R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; De Sews, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, March 2000
A;Reference number: 224487
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9
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A;Cross-references: EMBL:AB014601; NID:g3327215; PIDN:BAA31676.1; PID:g3327216
A;Experimental source: brain; clone HG01611
C;Genetics:
A;Note: KIAA0701
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                                                52 LRRYGYDSNLFSFESGRRCOTGQGIFAFKCARAEELFNMLQEIMQNNSINVVEEPVVERN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
     22;
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A,Introns: 68/3; 95/3; 138/3; 177/1; 251/3; 315/3
A;Note: F7A7.220
C;Superfamily: Arabidopsis thaliana hypothetical protein F7A7.220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 27.1%; Pred. No. 3.4; Matches 26; Conservative 11; Mismatches 34; Indels 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 630;
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     Indels
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  20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSFESGRRCQT -- GQGIFAFKCARAEELFNMLQEIM 95
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                                                                                                        211 IRRCGHSENFFFIEVGRSAVTGPGEFWMO-----
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A, Status: preliminary; translated from GB/EMBL/DDBJ
  Mismatches
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10.8%; Score 75.5; D.
Best Local Similarity 25.0%; Pred. No. 8;
Matches 36; Conservative 19; Mismatches
  7;
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A,Residues: 1-320 <BEV>
A,Cross-references: EMBL:AL161946
  21; Conservative
                                                                                                                                                                                                           249 MHETILEAMR 258
                                                                                                                                                              112 NHQTELEVPR 121
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Matches
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Nature 392, 353-358, 1998
                                                                                                                                                                              125 TP 126
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A; Note: F8F16.140
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A;Title: The interaction of bride of sevenless with sevenless is conserved between Dross A;Reference number: A47550; MUID:93281693; PMID:8506350
A;Sccssion: A47550
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-893 <HAR>
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                                                                     ---GKNLHPDVTGR--LLSQGVIAFRCPRSFMDQPLAEHFSPFRVQDMDLSNSVIEVSTL 210
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.Cross-references: EMBL:U65981; NID:g1513209; PID:g1513210; PIDN:AAC47833.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATPRISE homolog - Cryptosporidium parvum
C;Species: Cryptosporidium parvum
C;Species: Cryptosporidium parvum
C;Species: Cryptosporidium parvum
C;Date: 03-bec-1999 #sequence_revision 03-bec-1999 #text_change 18-Aug-2000
C;Date: 03-bec-1999 #sequence_revision 03-bec-1999 #text_change 18-Aug-2000
C;Accesion: T37308
R;Zhu, G; Keithly, J.S.
Mol. Biochem. Parasitol. 90, 307-316, 1997
A;Title: Molecular analysis of a P-type ATPase from Cryptosporidium parvum.
A;Reference number: Z31674, MUID:98156766; PMID:9497052
                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Drosophila virilis
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C;Accession: A47550
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                                         --LYTRKRDSVKWHYLCLRR
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A,Note: CppA-E1
C,Superfamily: ATPase nucleotide-binding domain homology
C,998-1193/Domain: ATPase nucleotide-binding domain homology <ATN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 1528;
                                                                                                                                                                                                                              ------MONNSINV-VEEPVVE---RNNHOTELEVPRIPRIPTIP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.5%; Score 73; DB 2; Length 893; 24.1%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
  Indels
                                                                                                                                                                                                                                                                                                                                                  bride of sevenless precursor - fruit fly (Drosophila virilis) N_i \Delta L ternate names: boss
  58;
                                         PDNHRNKFKVINVDDDGNELGSGIME-LTDTELI----
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ilarity 22.1%; Pred. No. 50;
Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19; Mismatches
    Mismatches
                                                                                                                            55 YGYDSNLFSFESGRRCQTGQGIFAFKCARA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: FlyBase:FBgn0013105
A;Introns: 14/3; 175/3; 324/3; 808/3
C;Keywords: transmembrane protein
    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 24.18
Matches 27; Conservative
    Conservative
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Best Local Similarity
Matches 27; Conserv
      40;
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      Matches
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A;Residues: 1-314 <AQF>
A;Cross-references: GB:AE000675; NID:g2982863; PIDN:AAC06488.1; PID:g2982868; GB:AE000657
A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D.E.; OV6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M.; Schon, O.; Hoheisel, J.; Mewes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeclicus. A,Reference number: A70300, MUID:98196666; PMID:9537320 A,Accession: D70313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 12-Jun-2003
C;Accesion: D70313
R;Deckert, G; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 YKIPTEYLSHQAFHVLLREAEEE--FGFEQA------GILRIPCEVA--VFESILKIME 144
                                                                                                                                                  68 RRCQTGQGIFAFKCAR---ABELFNMLQBIMQNNSINVVBBPVVBRNNHQTELEVPRTPR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 DSVKWHYL-----CLRRYGYDSNLFSFESGRRCQTGQGIFAFKCARAEELFNMLQEIMQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        shown
  67
                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
C;Accession: T04499
R;Bevan, M; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Hoheis submitted to the Protein Sequence Database, April 1998
A;Reference number: ZIS375
A;Accession: T04499
8 RNKFKVINVDDDGNELGSGIMELTDTELILYTRKRDSVKWHYLCLRRYGYDSNLFSFESG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
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Best Local Similarity 25.5%; 'Pred. No. 7.9;
Matches 28; Conservative 22; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :| :| :| | :| | :| DNKSDAYLTTQECRENATSEEVM---SYRHPSDCPRTPSHQPHSP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---INVVEEPVVERNNHQTELEVPRIP-RIPTIP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 189;
                                                                                                                                                                                                                                                                                                                                                                                                                 auxin-induced protein homolog F8F16.140 - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DIVPDNHRNKFKVINVDDDGNELGSG-----IMELIDTELIL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Residues: 1189 <BEV>
A,Residues: 1189 <BEV>
A,Residues: EMBL:AL021633
A,Cross-references: EMBL:AL021633
A,Experimental source: cultivar Columbia; BAC clone F8F16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Gene: ribF
C,Superfamily: uncharacterized conserved protein H10963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10,3%; Score 72; 24.2%; Pred. No. 4.2; rive 21; Mismatches
                                             567 RNNTKTLNISPIGNEQSPSFVEYQES--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            riboflavin kinase - Aquifex aeolicus
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Best Local Similarity 24.2%
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Job time: 20.6711 secs
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Tesistence protein RGC2B - garden lettuce
C;Species: Lactuca sativa (garden lettuce)
C;Species: Lactuca sativa (garden lettuce)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
R;Meyers, BC.; Shen, X.A.; Rohani, P.; Gaut, B.S.; Michelmore, R.W.
Plant Cell 10, 1833-1846, 1998
A;Title: Receptor-like genes in the major resistance locus of lettuce are subject to div
A;Reference number: 220861; MUID:99030191; PMID:9811792
                                                                                                                                                                                                                                                                                    probable myotubularin-like protein-tyrosine phosphatase - fission yeast (Schizosaccharom)
C;Species: Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: T37958
A;Acteus: preliminary; translated from GB/EMBL/DDBJ
A;Atatus: preliminary; translated from GB/EMBL/DDBJ
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Actus: 1-559 cSKE>
A;Cross-references: EMBL:298974; PIDN:CAB11639.1; GSPDB:GN00066; SPDB:SPAC19A8.03
A;Cross-references: Etrain 972h-; cosmid c19A8
C;Genetics:
C;Genetics:
A;Gene: SPDB:SPAC19A8.03
A;Map position: 1
A;Introns: 8/3; 200/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AF113948; NID:g4106968; PID:g4106970; PIDN:AAD03156.1
C;Genetics:
A;Introns: B89/3; 1058/3; 1282/3; 1526/3; 1803/3
A;Note: RGC2B
                            ---NMLQEIMQNNSINVVEEPVVERNN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 GNELGSGI-----MELTDTELILYTRKRDSVKWHYLCLRRYGYDSN----LFSFESGRRCQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 KVINVD--DDGNELGSGIMELTDTELILYTRKRDSVKW-HYLCLRRYGYDSNLFSFESGR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Species: Schizosaccharomyces pombe
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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                                                                                                                                                                                                                                                                                                                                                                       NHRNKFKVINVDDDGNELGSGIMELTDTELI-----LYTRKRDSVKWHYLCLRRYGY
                                                                                                                                      255 FGKKKRVLEVHILDFEGNLRGKRIK----VEFLKFIREEKKFSSVEELIQ 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                      -----DSNLFSFES---GRRCQTGQGIFAFKCARAEELFNMLQEIMQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.3%; Score 72; DB 2; Length 1810; 23.5%; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.3%; Score 72; DB 2; Length 559; 31.7%; Pred. No. 16; 11.7%; Indels tive 14; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|:
QCRD----FMFFCWRFQSTEDAMDVYDTLQELMSINNINNL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1810 <MEY>
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Matches 32; Conservative
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                               August 2, 2004, 09:23:08 ; Search time 13.6842 Seconds (without alignments) 494.666 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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MUE1_OCEIH
TRUA_SYNY3
VE1_HPV1A
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TRSI RAT
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Z200 HUMAN
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PAC_STRMU
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Match Length
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Perfect score:
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Maximum DB seq
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6 caulobacter	3 rhizobium m	2 saccharomy	2 schizosacch	0 mus musculı	5 homo sapier	8 brucella me	7 brucella su	9 sendai vin	6 methanococc		6 caenorhabdi
09aby	Q92sú3	P4056	003392	P9736	pyde0	OBydb	08£v1	P0682	058226	09kt0	, P34316
SYK CAUCR	LEPA RHIME	YIS2 YEAST	PCNA_SCHPO	ETV6 MOUSE	PA6B HUMAN	LEPA_BRUME	LEPA_BRUSU	RRPL_SENDE	Y816 METJA	DUSC_VIBCH	YKT5_CAEEL
щ	Н	Н	Н	Н	Н	Н	Н	1	Н	Н	Н
552	609	993	260	485	372	602	602	2048	297	323	358
9.5	9.5	9.5	9.4	9.4	9.3	9.3	9.3	9.3	9.2	9.2	9.5
	99	99	65,5	65.5	65	65	65	64.5	64	64	64
99											

ALIGNMENTS

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TISSUE=Brain;
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NAMES OF THE PROPERTY OF THE P
                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 AFKCARAEELFNMLQEIMQNNSIN---VVEEPVVERNNHQTELE---VPRIPRIPITP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Docking proteins interact with receptor tyrosine kinases and mediate particular biological responses.
SUBUNIT: Interacts with RasGAP and Abl.
TISSUE SPECIFICITY: Expressed in lung, spleen, skeletal muscle and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOX1 HUMAN STANDARD; PRT; 481 AA.
Q99704; Q901G6;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Docking protein 1 (p62(dok)) (Downstream of tyrosine kinase 1) (pp62).
                                                                                                                 -!- PTM: Constitutively tyrosine-phosphorylated (By similarity).
-!- PTM: Phosphorylated on tyrosine residues by the insulin receptor kinase. Results in the negative regulation of the insulin signaling pathway (By similarity).
-!- SIMILARITY: BELONGS TO THE DOK FAMILY.
-!- SIMILARITY: Contains 1 PH domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, U78818; AAB48827.2; -
EMBL, AF084363; AAC95339.1; -
EMBL, BC013066; AAH13066.1; -
MGD, MG1:893387; Dok1.
GO, GO:0007243; P:protein kinase cascade; IPI.
GO, GO:0007265; P:RAS protein signal transduction; IPI.
GO, GO:00071865; P:RAS protein signal transduction; IPI.
InterPro; IPR002404; InsIn_receptor protein tyrosine kin.
InterPro; IPR001849; PH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.8%; Score 145; DB 1; Length 482; 31.4%; Pred. No. 1.4e-07;
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PTB.
PHOSPHORYLATION (BY INSR)
SIMILARITY).
PHOSPHORYLATION (BY INSR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D -> N (IN REF. 4).
V -> A (IN REF. 3 AND 4).
C999C9FE0DA58EA3 CRC64;
                                                                                                    -!- DOMAIN: PTB domain mediates receptor interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52452 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam, PF02174, IRS; 1.
Pfam, PF00169; PH; 1.
SMART, SM00233; PH; 1.
SMART; SM00310; PTBI; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119
254
361
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482 AA;
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Best Local
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DOK1 HUMAN
DOK1 HUMAN
AC 099704,
DT 28-FEB
DT 28-FEB
DT 28-FEB
DT 28-FEB
OKING
CHOWN SE
OK HUMAN
CO BUKATYC
CO BUKATYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION OF TYR-362 AND TYR-398, AND MUTAGENESIS OF TYR-362 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spleen.
-!- DOMAIN: The PTB domain mediates receptor interaction.
-!- PTM: Constitutively tyrosine-phosphorylated.
-!- PTM: Phosphorylated on tyrosine residues by the insulin receptor kinase. Results in the negative regulation of the insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jeney, words, with 602919; -. GO, GO:0005515; F:protein binding; TAS. GO; GO:0005515; F:protein binding; TAS. GO; GO:0005166; P:cell surface receptor linked signal transdu. ..; (GO; GO:0007166; P:transmembrane receptor protein tyrosine Kin. ..; InterPro; IPR002404; Insln_receptorSl. InterPro; IPR001849; PH.
                                                                   Isoid=099704-1; Sequence=Displayed;
Name=2; Synonyms=p22Dookdel;
Isoid=099704-2; Sequence=VSP 003852, VSP 003853;
TISOID=099704-2; Sequence=VSP 003852, VSP and
                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=20398544; PubMed=10940083;
MEDLINE=20398544; PubMed=10940083;
Mubert P., Ferreira V., Debre P., Bismuth G.;
"Molecular cloning of a truncated p62Dokl isoform, p22Dokdel.";
Eur. J. Immunogenet. 27:145-148(2000).
                                                      Carpino N., Wisniewski D., Strife A., Marshak D., Kobayashi R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yu W., Sarginson J., Gibbs R.A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                signaling pathway.
-- SIMILARITY: BELONGS TO THE DOK FAMILY.
--- SIMILARITY: Contains 1 PH domain.
--- SIMILARITY: Contains 1 PTB domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEGEN; PF02174; IRS; 1.
Pfam; PF02169; PH; 1.
SMART; SM00233; PH; 1.
PROSITE; PS50003; PH_DOMAIN; FALSE_NEG.
SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=97160840; PubMed=9008160;
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                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=1; Synonyms=p62Dok1;
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RESULT
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                                                                                                                                                                                                                                                                                                     77
                                                                                                         Missing (in isoform 2).
/FIId=VSP 003853.
/FIId=VSP 003853.
Y-F: NO ASSOCIATION WITH NCK.
Y-F: NO ASSOCIATION WITH GAP; WHEN
ASSOCIATED WITH F-362.
MDGAVWEGPPFIQSQRFGTK -> RLPAQASATREREPRWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98148015; PubMed=9478921; MEDLINE=98148015; PubMed=9478921; MEDLINE=98148015; PubMed=9478921; Di Cristofano A., Caprpino N., Dunant N., Friedland G., Kobayashi R., Strife A., Wisnlewski D., Clarkson B., Pandolfi P.P., Resh M.D.; "Molecular cloning and characterization of p56dok-2 defines a new family of RasGAP-binding proteins:"; J. Biol. Chem. 273:4827-4830(1998).
-!- FUNCTION: Docking proteins interact with receptor tyrosine kinases and mediate particular biological responses.
-!- SUBUNIT: Interacts with RET (By similarity). Interacts with
                                                                   SQFWVTVQRTEAAERCGLHGSYVLR -> HVLFRGRPPLPL
RPWNLHLPDGTGK (in isoform 2).
/FIId=VSP_003852.
                                                                                                                                                                                                                                                                                                  24 GSGIMELIDIELILYTRKRDS -----VKWHYLCLRRYGYDSNLFSFESGRRCQTGQGIF
                                                                                                                                                                                                                                                                                                                      Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: Expressed in peripheral blood leukocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Docking protein 2 (p56(dok-2)) (Downstream of tyrosine kinase 2)
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                                                                                                                                                                                                                                                                                                                                                            78 AFKCARAEELFNMLQEIMQNNSINVVE---EPVVERNNHQTELEVPRTPRTP
                                                                                                                                                                                                                                                                                                                                                                             20.6%; Score 143.5; DB 1; Length 481; 29.5%; Pred. No. 2e-07; ive 20; Mismatches 50; Indels 9
                                                                                                                                                                                                 O (IN REF. 3).
E9D947831244BA6C CRC64;
                                         PHOSPHORYLATION (BY INSR) PHOSPHORYLATION (BY INSR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lymph nodes and spleen.
DOWAIN: PTB domain mediates receptor interaction.
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SIMILARITY: BELONGS TO THE DOK FAMILY.
SIMILARITY: Contains 1 PH domain.
SIMILARITY: Contains 1 PTB domain.
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splicing
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Genew; HGNC:2991; DOK2.
                                                                                                                                                                                                                52391 MW;
Alternative
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nes 33; Conservative
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398
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Phosphorylation;
DOMAIN 4
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398
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                         DOMAIN
MOD_RES
MOD_RES
VARSPLIC
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194 WPYRFLRRFGRDKVTFSFEAGRRCVSGEGNFEFETRQGNEIFLALEEAISAQKNAAPATP 253
                                                                                                                                                                                                                                                                                                                                                                                  47 WHYLCLRRYGYDSNLFSPESGRRCQTGQGIFAFKCARAEELFNMLQEIM--QNNSINVVE
                                                                                                                                                                                                                                                                                                                                          18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=89148015; PubMed=9478921;
MEDLINE=89148015; PubMed=9478921;
Di Cristofano A., Carpino N., Dunant N., Friedland G., Kobayashi R., Strife A., Wisniewski D., Clarkson B., Pandolfi P.P., Resh M.D.;
"Modecular cloning and characterization of p56dok-2 defines a new family of ResGAP-binding proteins.";
J. Biol. Chem. 273:4827-4830(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jones N., Dumont D.J.; "The Tek/Tie2 receptor signals through a novel Dok-related docking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98361297; PubMed=9697832; Nelms K., Snow A.L., Hu.Li J., Paul W.E.; Anematopoietic cell-specific rasGAP-interacting protein phosphorylated in response to cytokine stimulation."; Immunity 9:13-24(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOK2 MOUSE STANDARD; PRT; 412 AA.
070469; 070272; Q99Knl;
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Docking protein 2 (p56 (dok-2)) (Downstream of tyrosine kinase 2 related protein) (Dok-R) (IL-four receptor interacting protein)
GO; GO:0005515; F:protein binding; TAS.
GO; GO:0007166; P:cell surface receptor linked signal transdu.
InterPro; IPRO02404; Insln_receptorS1.
InterPro; IPRO01849; PH.
Pfam; PF02174; IRS; 1.
Pfam; PF00169; PH; 1.
SMART; SM00231; PH; 1.
SMART; SM00310; PFB1; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                              Length 412;
                                                                                                                                                                                                                                                                                              / Match 19.4%; Score 135; DB 1; Length 41:
Local Similarity 34.0%; Pred. No. 1.3e-06;
nes 33; Conservative 13; Mismatches 33; Indels
                                                                                                                                                                                                                                                        45548 MW; A8B08B07F0DA91EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 EPVVERNNHQTELEVPR------TPRTPTTP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 QP----QPATIPASLPRPDSPYSRPHDSLPPPSPTTP 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98435849; PubMed=9764820;
                                                                                                                                                                                                              PH.
PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oncogene 17:1097-1108(1998).
                                                                                                                                                                                                              114247
                                                                                                                                                                                                                                                        412 AA;
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                                                                                                                                                                                          Phosphorylation.
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                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                      DOMAIN
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A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., A Raha S.S., Loquellano N.B., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., Mogwan P.J., McKernan K.J., Malak J.A., Gunaratne P.H., Richards S., Horley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., A Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Rodrigues S., Sonchez A., A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., A Butcerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF030627; AAC31315.1; -.
EMBL; AF03117, AAC13266.1; -.
EMBL; AF055583; AAC7666.1; -.
EMBL; BC004590; AAC7666.1; -.
EMBL; BC004590; AAC7666.1; -.
EMBL; BC004590; AAC766.1; -.
EMBL; BC004590; AAC766.1; -.
GO; GO:0005069; Fitransembrane receptor protein tyrosine kin. . .; IPI.
GO; GO:0007169; P:transembrane receptor protein tyrosine kin. . .; IPI.
InterPro; IPR002404; Insln_receptorSl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gell Biol. 154:345-354(2001).

-!- FUNCTION: Docking proteins interact with receptor tyrosine kinases and mediate particular biological responses. May modulate the cellular prolliferation induced by IL-4, as well as IL-2 and IL-3.

-!- SUBUNIT: Interacts with RasGAP, TEK/TIE2 receptor and EGF receptor. Interacts with RET.

-!- TISSUE SPECIFICITY: Expressed in lung and spleen.

-!- DOMAIN: PTB domain mediates receptor interaction.

-!- PTM: Tyrosine phosphorylated.

-!- SIMILARITY: Contains 1 PTB domain.
                                                                                                                                                                                                                                                                                                                     INTERACTION WITH RET.
MEDLINE=21363571; PubMed=11470823;
Grimm J., Sachs M., Britsch S., Di Cesare S., Schwarz-Romond T.,
Alitalo K., Birchmeier W.;
"Novel p62dok family members, dok-4 and dok-5, are substrates of the
c-Ret receptor tyrosine kinase and mediate neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.4%; Score 128; DB 1; Length 412; 35.7%; Pred. No. 7e-06; tive 12; Mismatches 28; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02AC02530DBED053 CRC64;
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PTB.
A -> T (IN REF. 4).
L -> F (IN REF. 2).
P -> T (IN REF. 2).
MISSING (IN REF. 4).
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Pfam; PF02169; PH; 1.
SMART; SM00233; PH; 1.
SMART; SM00310; PTBI; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45522 MW;
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249
245
330
347
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REAL MEDLINE-21648749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
Beloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
Deloukas P., Matthews L.H., Ashurst J., Bardel L.M., Beare D.M.,
Balley J., Blook R.F., Bares K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Ghapman J.C., Clamp M., Clark S.Y., Clark S.Y., Clark C., Carter N.P.,
Choley V.E., Collier R.E., Connor R.E., Corby N.R.,
Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
A Ellington A.G., Frankland J.A., Fraser A., French L. Dunn M.,
RA Ellington A.G., Harley J.L., Heath P.D., Ho S., Holden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA MY M.P., Kimberley A.M., Kingh R., Knights A., Laird G.K., Lawlor S.,
Lehvaeslaino M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Mine S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Mine S.A., Mistry D., Moore M.J.F., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showhkeen R., Silms S.,
Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Tracey A., Tromans A.C., Vaudin M., Wallis J.M.,
RA Mitchead S.L., Mittaker P., Willey D.L., Milliams L., Williams S.A.,
Whitehead S.L., Mittaker P., Willey D.L., Williams L., Williams S.A.,
RA Mining L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
                           244
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diactochenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The DNA sequence and comparative analysis of human chromosome 20."; Nature 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
Favre C., Gerard A., Nunes V.A.;
"Dock and DOK5: new DOK-related genes expressed in human T cells.";
Submitted (JAN-2002) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                         (Protein dok-5)
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
SEQUENCE FROM N.A. (ISOFORM 1).
Luo W.Q., Chen J.H., Huang X.W., Zhou Y., Zhou H.J., Hu S.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                   DOKS HUMAN STANDARD; OBEZ4; 306 AA.
O9P104; O8TEW7; Q96f113; OBEZ4; O9NQF4; O9Y411;
28-FEB-2003 (Rel. 41, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Docking protein 5 (Downstream of tyrosine kinase 8)
DOKS OR C20ORF180.
Homo sapiens (Human)
                                                                        107 VVERNNHQTELEVPRIPRI-PTIP 129
                                                                                                                     245 AVOKN -- ATPSGPPSLPATGPMMP 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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Conservative

Best Local Similarity Matches 30; Conserv

Query Match

14;

153 GECALQITYEYICLWDVQNPRVKLISWPLSALRRYGRDTTWFTFBAGRMCETGEGLFIFQ 212

81 CARABELFNML------QEIMQNNSINVVEEPVVER-NNHQTELEVPRT 122

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                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

-!-FUNCTION: Docking proteins interact with receptor tyrosine kinases and mediate particular biological responses. Functions in RET-mediated neurite outgrowth and plays a positive role in activation of the MAP kinase pathway. Putative link with donwstream effectors of RET in neuronal differentiation (By similarity).
-!-SUBWIT: Interacts with phosphorylated RET. In contrast to other DOK proteins, it does not interact with RASGAP (By similarity).
-!-ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isola-g9P104-2; Sequence=VSP 003854;
Note=No experimental confirmation available;
Note=No Bomain mediates receptor interaction (By similarity).
SIMILARITY: BELONGS TO THE DOX FAMILY.
SIMILARITY: Contains 1 PH domain.
SIMILARITY: Contains 1 PTB domain.
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Halle S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Expansion J.W., Krzywinski M.T., Skalska U., Smailus D.E., Schnertion and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              î
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                                                                                                                                                                                                                                                         SEQUENCE OF 42-306 FROM N.A. (ISOFORM 1).
TISSUE=Kidney;
Ottenwaelder B., Obermaier B., Mewes H.-W., Gassenhuber J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Missing (in isoform 2).
/FIId=VSP 003854.
SAALAIAEQH -> LLQMKMSERA.
2F259529E8B06BDB CRC64;
                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=09P104-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM0023; PH; 1.
SMART; SM00310; PTB1; 1.
PROSITE; PS50003; PH DOMAIN; FALSE_NEG.
Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:16173; DOKS.
InterPro; IPR002404; Insln_receptorS1.
InterPro; IPR0010849; PH.
Pfam; PF00174; IRS; 1.
Pfam; PF00169; PH; 1.
                                                                                                                                                                                                      human and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AF132732; AAF66443.1; --
EMBL; AF46636; AAL74194.1; --
EMBL; AL118501; CAC00469.1; --
EMBL; AL162292; CAC32860.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 234 S.
306 AA; 35463 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; BC008992; AAH08992.1;
EMBL; AL050069; CAB43255.1;
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                                                                                                                                                                                                                                                                                                                        Wiemann S.;
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SEQUENCE
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Kawal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Kawal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Bromstein M.J., Bult C., Fletcher C., Fuljita M., Gariboldi M.,

Bromstein M.J., Bult C., Fletcher C., Fuljita M., Gariboldi M.,

By Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Rymshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

M. Wannian-Boris A., Yoshida K., Rasegawa Y., Kawaji H., Kohtsuki S.,

M. Wannian-Boris A., Yoshida K., Rasegawa Y., Kawaji H., Kohtsuki S.,

M. Wannian-Boris A., Yoshida K., Rasegawa Y., Kawaji H., Kohtsuki S.,

M. Wannian-Boris A., Washida K., Rasegawa Y., Kawaji H., Kohtsuki S.,

M. Wannian-Boris A., Washida K., Rasegawa Y., Kawaji H., Kohtsuki S.,

M. Wannian-Boris A., Washida K., Rasegawa Y., Kawaji H., Kayanian M.,

M. Wannian-Boris A., Washida K., Rasegawa Y., Kawaji H., Kayanian M.,

M. Wannian-Boris A., Washida K., Rasegawa Y., Kawaji H., Kayanian M.,

M. Wannian-Boris A., Washida K., Rasegawa Y., Kawaji H., Kayanian M.,

M. Wannian-Boris A., Wang K., Kawaji H., Kayanian M.,

M. Wannian-Boris A., Yoshida K., Kayanian M., Kayanian M.,

M. Wannian-Boris A., Yoshida K., Kayanian M., Kayanian M.,

M. Wannian-Boris A., Yoshida K., Kayanian M., Kayanian M.,

M. Wannian-Boris A., Yoshida K., Kayanian M., Kayanian M.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21363571; PubMed=11470823; Grim J., Sachs M., Britsch S., Di Cesare S., Schwarz-Romond T., Alitalo K., Birchmeier W.; Alitalo K., Elrchmeier W.; "Novel p52dok Emmily members, dok-4 and dok-5, are substrates of the c-Ret receptor tyrosine kinase and mediate neuronal
                                                                                                                                                                                                                        DOKS MOUSE STANDARD; PRT; 306 AA.
O912M9; Q9CSM6;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
Docking protein 5 (Downstream of tyrosine kinase 5) (Protein dok-5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
: | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cell Biol. 154:345-354(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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                                                                                                                                                RESULT
DOK5_MO
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<u>ب</u> 80

Gaps

15;

17.9%; Score 124.5; DB 1; Length 306; 26.3%; Pred. No. 1.1e-05; tive 29; Mismatches 40; Indels 15

Conservative

Similarity

Local Sim

Matches

Query Match

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Query Match
Best Local Simi
Matches 24;
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MEDLINE=94067102; PubMed=7504175;
Sun X.J., Crimmins D.L., Myers M.G., Miralpeix M., White M.F.,;
"Pleiotropic insulin signals are engaged by multisite phosphorylation
of IRS-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE=93352637; PubMed=8349691;
Tanasijevic M.J., Myers M.G., Thoma R.S., Crimmins D.L., White M.F.,
Sacks D.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Sprague-Dawley, TISSUE-Liver,
MEDLINE-91927824, PubMed=1649180;
Sun X.J., Rothenberg P. Kahn C.R., Backer J.M., Araki B.,
Wilden P.A., Cahill D.A., Goldstein B.J., White M.P.;
"Structure of the insulin receptor substrate IRS-1 defines a unique signal transduction protein.";
Nature 352:73-77(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 TRDGEAIYQKVHSAALAIAEQHERLLQSVKNSMLQMKKSERAASLSTVVPLPRS 266
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                                                                                                                                         EMBL, AF418208; AAL14627.1; ---
EMBL, AK012430; BAB28233.1; ---
EMBL, AK012430; BAB28233.1; ---
MOD, MG1:1924079; Dok5.

GO; GO:0000165; F:transmembrane receptor protein tyrosine kin.
GO; GO:0000165; P:MAPKKK cascade; IDA.
GO; GO:0007169; P:neurogenesis; IDA.
GO; GO:0007169; P:neurogenesis; IDA.
InterPro; IPR002404; Insln_receptor protein tyrosine kin.
InterPro; IPR001849; PH.
Pfam; PF02174; IRS; 1.
Pfam; PF02174; IRS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.5%; Score 121.5; DB 1; Length 306; 26.3%; Pred. No. 2.3e-05; ive 28; Mismatches 41; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35453 MW; 7889802FBEAC04A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                              Pfam; Provider; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol. Cell. Biol. 13:7418-7428(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insulin receptor substrate-1.
IRS1 OR IRS-1.
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nes 30, Conserv
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DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2001 (Rel. 40, Last annotation update)
DE Zino-finger protein DPF3 (cer-d4).
GN CERD4.
OS Gallus Gallus (Chicken).
OC Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, OC Archosauria, Aves; Neognathae, Galliformes; Phasianidae, Phasianinae, NCBI TaxID=9031;
NCBI TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 LRRYGYDSNLFSFESGRRCQTGQGIFAFKCARAEELFNMLQEIMQNNSINVVEEPVVERN 111
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kinase II.";
J. Biol. Chem. 268:18157-18166(1993).
I. Biol. Chem. 268:18157-18166(1993).
I. FUNCTION: May mediate the control of various cellular processes by insulin. When phosphorylated by the insulin receptor binds specifically to various cellular proteins containing SH2 domains such as phosphatidylinositol 3-kinase p85 subunit or GRB2.
I. SIMILARITY: Contains I PH domain.
I. SIMILARITY: Contains I PTB domain.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131178 MW; A274BC7540CA85C5 CRC64;
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(BY INSR)
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Pred. No. 1.8;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 IRRCGHSENFFFIEVGRSAVTGPGEFWMQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP, P35568, 11RS.
Interpro, IPR002404; Insln_receptorS1.
Interpro, IPR001849; PH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 NHQTELEVPRT-----PRT 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50003; PH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.8%;
30.0%;
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SMART; SMO0233; PH; 1.
SMART; SMO0310; PTBI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X58375; CAA41264.1; -.
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881
1200
99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02174; IRS; 1.
Pfam; PF00169; PH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S16948; S16948.
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202 PKRKNR-----PRGRPKTPT 216
                         108 VERNNHQTELEVPR-TPRTPT 127
                                                                                                                             Z200 HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 YGYDSNLFSFESGRRCQTGQGIFAFKCARAEELFNMLQEIMQN-----NSINVVEEPV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 SRLKLLEIKPETSHLPGKTELITETEFITKMSVDLRRFLSCKLYTSEVD-----LPLKK 144
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LFCDDCDRGYHNYCLNPPVFBPPEGSWSCHLCRELLRERAS
AFGFQA -> AHLGREGRRDEAAPTRTTEDLFGSTSESDTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 NKFKVINVDDDGNELGSGIMELTDTELI-------LYTRKRDSVKWHYLCLRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45; Indels 37; Gaps
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                                                                                                                                                                                                                                                                                                                   VSP_005615, VSP_005616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Missing (in isoform 2, isoform 3 and
SEQUENCE FROM N.A. (ISOPORMS 1; 2; 3 AND 4).
MEDLINE=21833813; PubMed=11845289;
Minkina N.N., Mertsalov I.B., Kulikova D.A., Alimova-Kost M.V.,
Simonova O.B., Korochkin L.I., Kiselev S.L., Buchman V.L.;
"Cerd4, third member of the d4 gene family: expression and
organization of genomic locus.";
Mamm. Genome 12:862-866(2001).
-! FUNCTION: Probably involved in RNA transcription.
-! SUBCELLULAR LOCATION: Muclear and cytoplasmic (Potential).
-! ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWART; SM00249; PHD; 2.
SWART; SM00355; ZnF C2H2; 1.
PROSITE; PS01359; ZF PHD 2; 2.
PROSITE; PS0006; ZINC_FINGER_C2H2_1; 1.
PROSITE; PS010157; ZINC_FINGER_C2H2_1; 1.
Transcription regulation; Zinc_finger; Nuclear protein; Repeat; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 80.5; DB 1; Length 427; Pred. No. 0.72;
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                                                                                                                                                                                                                                                Isold=P58270-2; Sequence=VSP_005614, VSP_005615;
                                                                                                                                                                                                                                                                                  IsoId=P58270-3; Sequence=VSP_005614, VSP_005616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isoform 3 and isoform 4)/FTId=VSP 005616.
                                                                                                                                                                                                                                                                                                                 IsoId=P58270-4; Sequence=VSP_005614, VSP_0056-!- SIMILARITY: Belongs to the requiem/DPF family.-!- SIMILARITY: Contains 2 PHD-type zinc fingers.
                                                                                                                                                                              Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'FTId=VSP 005614.
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PHD-TYPE 2. -
                                                                                                                                                                                                               IsoId=P58270-1; Sequence=Displayed;
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EMBL, AF362755; AAK51967.1; -.
EMBL, AF362756; AAK51970.1; -.
EMBL, AF362755; AAK51970.1; -.
InterPro, IPR007087; Znf C2H2.
InterPro, IPR001965; Znf PHD.
Pfam, PF00628; PHD, 2.
Pfam, PF00626; zf-C2H2; 1.
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A Bernot A, Clepet C., Dasilva C., Devaud C., Petit J.-L.,
Caloustian C., Cruaud C., Samson D., Pulcini F., Weissenbach J.,
Heilig R., Notanicola C., Damingo C., Rozenbaum M., Benchetrit E.,
A Topaloglu R., Dewalle M., Dross C., Hadjari P., Duyont M.,
Demaille J., Touitou I., Smaoui N., Nedelec B., Mery J.-P.,
Chabbouni H., Delpech M., Grareau G.,
I. A candidate gene for familial Mediterranean fever.";
I. A candidate gene for familial Mediterranean fever.";
I. Subcellular Location: Nuclear (Probable)
C. -- SUBCELLULAR LOCATION: Nuclear (Probable)
C. -- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS, WEAKLY EXPRESSED
C. -- TISSUE SPECIFICITY: PROSTATE, OVARY, SMALL INTESTINE COLON AND
PERIPPERAL BLOOD LEUKOCYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deng Z., Centola M., Chen X., Sood R., Vedula A., Fischel-Ghodsian N.,
Kastner D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kastner D.L.;
"Identification of two Kruppel-related zinc finger genes (ZNF200 and
ZNF210) from human chromosome 16p13.3.";
Genomics 53:97-103(1998).
                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
2200 HUMAN STANDARD; PRT; 394 AA. P99187; 015361; 2004 MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) 2inc finger protein 200. Zinc finger protein 200. HUMBOO OR ZNEMF.
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MEDLINE=99005537; PubMed=9787081;
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9
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                                                                                                                                                       262 ESSYLISHQ---RTHTGEK--PYDCNHCGKSFNHKTNLNKHERIHTGEKPYSCSQCGKNF 316
                                                                                                                                2 TVPDNHRNKFKVINVDDDGNELGSGIMELT---DTELILYTRKRDSVKWHY--LCLRRYG 56
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-!- FUNCTION: May mediate the control of various cellular processes by insulin. When phosphorylated by the insulin receptor binds specifically to various cellular proteins containing SH2 domains such as phosphatidylinositol 3-kinase p85 subunit or GRB2.
-!- SIMILARITY: Contains 1 PH3 domain.
                                                                                       Gaps
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Araki E., Haag B.L. III, Kahn C.R.;
Cloning of the mouse insulin receptor substrate-1 (IRS-1) gene and complete sequence of mouse IRS-1.";
Biochim. Biophys. Acta 1221:353-356(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93192326; PubMed-8448209;
Keller S.R., Aebersold R., Garner C.W., Lienhard G.E.;
"The insulin-elicited 160 kDa phosphotyrosine protein in mouse
adipocytes is an insulin receptor substrate 1: identification by
                                                                                     23;
                                    11:4%; Score 79.5; DB 1; Length 394; 20.8%; Pred. No. 0.83; ive 32; Mismatches 48; Indels 2:
45402 MW; 8EB613F0F5523377 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISI_MOUSE STANDARD; PRT; 1233 AA. P35569.
P35569.
P35569.
P3757.
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EMBL; X6972; CAA49378.1; -.
PIR; S30185; S30185.
PDB; 1AYB; 31-AUG-94.
MGD; MGI:99454; Irs1.
Interpro; IPR002404; Ins1nreceptorS1.
Interpro; IPR001849; PH.
Pfam; PF02174; IRS; 1.
Pfam; PF00169; PH; 1.
PRINTS; PR00628; INSULINRSI.
SMART; SM00233; PH; 1.
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                                                              Best Local Similarity 20.8%
Matches 27; Conservative
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52 LRRYGYDSNLFSFESGRRCQTGQGIFAFKCARAEELFNMLQEIMQNNSINVVEEPVVERN 111
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MEDLINE=9329738; PubMed=8513971;
ARAKI E., Sun X. Haag B.L. III, Chuang L.M., Zhang Y.,
Yaray-Feng T.L., White M.F., Kahn C.R.;
"Human skeletal muscle insulin receptor substrate-1. Characterization of the cDNA, gene, and Ochromosomal localization.";
Diabetes 42:1041-1054(1990)
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MEDLINE-92181456; PubMed=1311924;
Nishiyama M., Wands J.R.;
"Cloning and increased expression of an insulin receptor substrate-1-
like gene in human hepatocoellular carcinoma.";
Biochem. Biophys. Res. Commun. 183:280-285(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22; Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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PHOSPHORYLATION (BY INSR)
(BY SIMILARITY).
MISSING (IN REF. 2).
H -> R (IN REF. 2).
MW; COE992D890DADD87 CRC64;
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(BY SIMILARITY).
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01-JUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Insulin receptor substrate-1 (IRS-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.2%; Score 78; DB 1
30.0%; Pred. No. 4.8;
tive 7; Mismatches
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SMART; SM00310; PTBI; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
FT DOMAIN 12 115
FT DOMAIN 152 262 PF.
DOMAIN 675 680 P
"ALN 872 877
1119 1128
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1233 AA; 130723
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Best Local Similarity 30.0
Matches 21; Conservative
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3MBL; S85963; AAB21608.1; -.
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                                     REDIENE=22388257; PubMed=12477932;

REDIENE=22388257; PubMed=12477932;

REDIENE=22388257; PubMed=12477932;

Retausher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Bactow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Bactow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A staplecon M. Soares M.B. R., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.W., McKernan K.J., Malek J.A., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Vilalon D.K., Munny D.W., Sodergren E.J., Lu X., Gibbs R.A.,

Rahesley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Reterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length

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Consoli A., Mariani-Costantini R., Caramia F.G., Cama A., Battista P.;
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with noninsulin-dependent diabetes mellitus.";
Hum. Mutat. 7:364-366(1996).
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Zhou M.-M., Huang B., Olejniczak B.T., Meadows R.P., Shuker S.B.,
Anyazaki M., Trueb T., Shoelson S.E., Fesik S.W.;
Miyazaki M., Trueb T., Shoelson S.E., Fesik S.W.;
Structural basis for IL-4 receptor phosphopeptide recognition by the IRS-1 PTB domain.";
Nat. Struct. Biol. 3:388-393(1996).

-!- FUNCTION: May mediate the control of various cellular processes by insulin. When phosphorylated by the insulin receptor binds specifically to various cellular proteins containing SH2 domains such as phosphatidylinositol 3-kinase p85 subunit or GRB2.
-!- DISEASE: POLYMORPHISMS IN IRS1 MAY BE INVOLVED IN THE ETIOLOGY OF A SUBSET OF LATE-ONSET NON-INSULIN-DEPENDENT DIABETES MELLITUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANTS NIDMM TYR-1043 AND TYR-1085.

Mammarella S., Creati B., Esposito D.L., Arcuri P., della Loggia F.,
Capani F., Mariani-Costantini R., Caramia F.G., Battista P., Cama A.;
"Novel allele of the insulin receptor substrate-1 bearing two
non-conservative amino acid substitutions in a patient with
Hum. Mutat. 11:411-411(1998).
                                                                                                                                                                                                                                                                                                                                                                                                 ς;
Ω
                                                                                                                                                                                                                                                                                                                                                                     VARIANTS PRO-512 AND ARG-971.
MEDLINE-93390176; PubMed-8104271;
Almind K., Bjoerbaek C., Vestergaard H., Hansen T., Echwald
                                                                                                                                                                                                                                                                                                                                                                                                                       "Aminoacid polymorphisms of insulin receptor substrate-1 in
non-insulin-dependent diabetes mellitus.";
Lancet 342:828-832(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Contains 1 PH domain. SIMILARITY: Contains 1 PTB domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRUCTURE BY NMR OF 157-267
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                                                                                                                                                                                                                                                                                                                                                                                                                 Pedersen O.;
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EMBL; 852399; AAH53895.1; -.

REMBL; 15.MAY-97.

REMBL; 10.MOV-99.

REMBL; 10.M
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(BY SIMILARITY).
(BY SIMILARITY
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S -> F (in dbSNP:1801120).

/FTIG=VAR 014855.

S -> G (in dbSNP:1801277).

/FTIG=VAR 014856.

G -> R (in dbSNP:1801277).

/FTIG=VAR 016856.
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C -> Y (IN NIDDM).
/FTId=VAR 005303.
G -> GG (IN REF. 2).
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PTB.
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                                                                                                                                      128 DAVPANIPVSAKIRLGWENPEDCFEIVDAIQSAGANELTVHARTKQGGYKASEIKWEYIN 187
                                                                                                                                                                                  1 DIVPDNHRNKFKV---INVDDDGNELGSGIMELIDTELILYTR-----KRDSVKWHYLC
                                                                                                                                                                  LRRYGY------DSNLFSFESGRRCQTGQGIFAFKCARAEELFNM--LQEIMQNNSINVV
               tRNA processing; Oxidoreductase; Flavoprotein; FAD; Complete proteome
SEQUENCE 322 AA; 36586 MW; 1F501F7C733D924B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The interaction of bride of sevenless with sevenless is conserved between Drosophila virilis and Drosophila melanogaster."; Proc. Natl. Acad. Sci. U.S.A. 90:5047-5051(1993).
-!- FUNCTION. Acts as a ligand for sevenless tyrosine-kinase receptor during eye development.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila virilis (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota,
Noptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                       DB 1; Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93281693; PubMed=8506350;
Hart A.C., Harrison S.D., van Vactor D.L. Jr., Rubin G.M.,
Zipursky S.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BRIDE OF SEVENLESS PROTEIN.
EXTRACELLULAR (POTENTIAL).
                                                                                    .09
                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Bride of sevenless protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.6%; Score 73.5; DE 22.8%; Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                     893 AA.
                                                                                  26; Mismatches
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PIR; A47550; A47550.
FlyBase; FBgn0013105; Dvir\boss.
Interpro; IPR002956; Bride of 7less.
Interpro; IPR000337; GPCR_Mgr.
Pfam; PF00003; 7tm_3; 1.
                                                                                                                                                                                                                        104 EEPVVERNNHQTELEV 119
                                                                                                                                                                                                                                                  246 WSDVVDLLIYYSKFEM 261
  PROSITE; PS01136; UPF0034; 1.
                                                                 Local Similarity 22.89
                                                                                                                                                                                                                                                                                                                     STANDARD;
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SIGNAL
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                                                        Query Match
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                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                               52 LRRYGYDSNLFSFESGRRCQTGQGIFAFKCARAEELFNMLQEIMQNNSINVVEEPVVERN 111
                                                                                                                                                                                                                                                                                                                                                                       211 IRRCGHSENFFFIEVGRSAVTGPGEFWMQ---------VDDSVVAQN 248
                                                                                                                                                                                                                                                                                                                     22; Gaps
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SECONDARD FROM N.A.

MEDLIND=225608454; PubMed=12620739;
MEDLIND=225608454; PubMed=12620739;
MEDLIND=225608454; PubMed=12620739;
Makino K., Goshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Tijima Y., Najima M., Nakamo M., Yamashita A., Kubota Y.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.,
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
Lancet 361:743-749(2003).

-!-FUNCTION: Catalyzes the synthesis of dihydrouridine, a modified
base found in the D-loop of most tRNAs (By similarity).
-!- COFACTOR: FAD (By similarity).
-!- SIMILARITY: Belongs to the dus family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                         DB 1; Length 1242;
                                                                                                                                                                                                                                                                                                                     20; Indels
                                                                                                                                                                                                                                                               131590 MW; 3COEFD9E32B3E64A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2hhydrouridine synthase C (EC 1.-.-.).
 R (IN REF. R (IN REF.
                                                                                                                                                                                                                                                                                        Score 78; DB 1
Pred. No. 4.8;
7; Mismatches
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γ ^
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Pfam; PF01207; Dus; 1.
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 30.0
Matches 21; Conservative
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Vibrio parahaemolyticus.
                                                                                                                                                                                                                                                                                                                                                                                                                               249 MHETILEAMR 258
                                                                                                                                                                                                                                                                                                                                                                                                    112 NHQTELEVPR 121
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                                                                                                                                                                                                                                                263 26
1242 AA;
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 NCBI_TaxID=670;
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CONFLICT
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SEQUENCE
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DUSC_VIBPA
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                                                                                                                                                                                                                                              310
                                                                                                                                                                                                               26
                                                                                                                                                                                                                                          253 GEKIAS -- VEIVTETLDIYNEFMDAARQEHMCLMHFKSDDNVYILFGNKMANHFKENGTV
                                                                                                                                                                                                             20 GNELGSGIMELTDTELILYTRKRDSVKWHYLCLRRYGYDSN---LFSFESGRRCQTGQGI
                                                                                                                                                                                Gaps
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GO: 00.0005677; F:DNA binding; NAS.
GO: 00.0008270; F:Zinc londing; NAS.
GO: 00.0008270; F:zinc londing; NAS.
GO: 00.0008250; P:zinc londing; NAS.
InterPro: IPR007080; ZRAB.
InterPro: IPR007087; Znf_CZH2.
InterPro: IPR007086; Znf_CZH2.
Pfam; PP001352; KRAB. 1.
Pfam; PF00096; Zf-CZH2. 10.
Pfam; PF00096; Zf-CZH2. 10.
PRINTS; PR00048; ZINCFINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Bone marrow;
MEDLINE=20054457; PubMed=10585455;
Han Z.-G., Zhang Q.-H., Ye M., Kan L.-K., Gu B.-W., He K.-L.,
Shi S.-L., Zhou J., Fu G., Mao M., Chen S.-J., Yu L., Chen Z.;
"Molecular cloning of six novel Kruppel-like zinc finger genes from hematopoietic cells and identification of a novel transregulatory
                                                            (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                                                                                                                                                                                           77 FAFKCARAEELFINMLQEIMQNNSINVVEEPVVERNNHQTELEVPRTPTT 128
                                                                                                                                                                                                                                                                                                J. BENNOTION: May function as a transcription factor.
-!- FUNCTION: May function as a transcription factor.
-!- SUBCELDULAR LOCATION: Nuclear (Probable).
-!- SINILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                16;
                                (POTENTIAL) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 Rel. 42, Last annotation update)
Zinc finger protein 257 (Bone marrow zinc finger 4) (BMZF-4)
2NF257 OR BMZF4.
                                                                                                                                             Score 73; DB 1; Length 893;
Pred. No. 11;
                                                                                                                                                                                50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                               183 N-LINKED (GLCNAC. . .) (PO 307 N-LINKED (GLCNAC. . .) (PO 328 N-LINKED (GLCNAC. . .) (PO 482 N-LINKED (GLCNAC. . .) (PO 99939 MW, ABB9D4C21DB680C3 CRC64;
             CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                           535 AA
                                                                                                                                                                                19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Contains 1 KRAB domain.
                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF070651; AAD20957.1; -.
HSSP; P08047; 1SP2.
Genew; HGNC:13498; ZNF257.
                                                                                                                                                                                                                                                                                                                                                                                                                         [6-OCT-2001 (Rel. 40, Created)
[6-OCT-2001 (Rel. 40, Last seq
                                                                                                                                               10.5%;
24.1%;
                                                                                                                                                                                27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
 772
893
183
307
328
471
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                                                                                                                 Ą.
                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC:1345
MTM; 606957; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain KRNB.";
                                                                                                                893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
                                                                                                                                                                                                                                                                                                            311
                                                                               CARBOHYD
CARBOHYD
SEQUENCE
TRANSMEM
DOMAIN
                                CARBOHYD
                                              CARBOHYD
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                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 CCKAFKWSSALTTLTQHKRIHTGEK--PYKCEECGKAFNQSSALTRHKMIHTGEKPFQCE 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDIANGE 2664461; MEDIINE 89313732; PubMed 2664461; Schiestl R.H., Reynolds P., Prakash S., Prakash L.; Schiestl R.H., Reynolds P., Prakash S., Prakash L.; Gloning and sequence analysis of the Saccharomyces cerevisiae RAD9 gene and further evidence that its product is required for cell cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE-91061763; PubMed=2247073;
Weinert T.A., Hartwell L.H.;
"Characterization of RAD9 of Saccharomyces cerevisiae and evidence
that its function acts posttranslationally in cell cycle arrest after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                     SMART; SM00349; KRAB; 1.

PROSITE; PS50035; ZnF C2H2; 12.

PROSITE; PS500028; ZINC FINGER C2H2 1; 10.

PROSITE; PS50157; ZINC FINGER C2H2 2; 12.

PROSITE; PS50157; ZINC FINGER C2H2 2; 12.

MUCLear protein; Repeat.

KRAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Fungi, Ascomycota; Saccharomycotina, Saccharomycetes; Saccharomycetales; Saccharomycetaceae, Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 535;
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Murphy L., Harris D., Barrell B.G., Rajandream M.A.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22DC5B0C4613BC51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98429491; PubMed=9755168; Vialard J.E., Gilbert C.S., Green C.M., Lowndes N.F.;
                                                                                                                                                                                                                                                                                                    (DEGENERATE)
                                                                                                                                                                                                                                                                                                                                                                                                     (ATYPICAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT, 1309 AA. P1477; 004920, 01-APR-1990 (Rel. 14, Created) 01-APR-1990 (Rel. 14, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) DNA repair protein RAD9. PAS-1990 (NRS-100-000) NRS-100-000 (NRS-100-0000) NRS-100-000 (NRS-100-0000) NRS-100-000 (NRS-100-0000) NRS-100-000 (NRS-100-0000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Pred. No. 7.4;
18; Mismatches
                                                                                                                                                                                                                       C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE
C2H2-TYPE.
C2H2-TYPE.
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C2H2-TYPE
C2H2-TYPE.
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. Cell. Biol. 10:6554-6564(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arrest induced by DNA damage.";
Mol. Cell. Biol. 9:1882-1896(1989)
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  ω,
  Znf_C2H2;
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18; Conservative
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229
229
257
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344
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403
483
459
855 AA,
PD000003;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          390 TQIVNNPRTQEMPLDSISIDTQPLSKSFNTETNNELETQIIVSCLSQGISAQKGPVFHST 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28
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GO; GO:0005634; C:nucleus; IC.
GO; GO:000515; F:protein binding; IDA.
GO; GO:000077; P:DNA damage response, signal transduction re. . .; IMP.
GO; GO:0006589; P:nucleotide-excision repair; IMP.
GO; GO:0006589; P:nucleotide-excision repair; IMP.
GO; GO:0006589; P:nucleotide-excision repair; IMP.
GO; GO:00074; P:regulation of cell cycle; IGI.
InterPro; IPRO01357; BRCT.
Ffam; PRO0533; BRCT; 1.
SMART; SM00292; BRCT; 1.
SMART; SM00292; BRCT; 1.
Cell cycle; DNA damage; DNA replication inhibitor; Nuclear protein; Phosphorylation; 3D-structure.
DOMAIN.
994 1122
BRCT.
DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
"The budding yeast Rad9 checkpoint protein is subjected to Mec1/Tell-dependent hyperphosphorylation and interacts with Rad53 after DNA damage.";
EMEO J. 17:5679-5688 (1998).
-:- FUNCTION: Essential for cell cycle arrest at the G2 stage following DNA damage by X-irradiation or inactivation of DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
10.3%; Score 71.5; DB 1; Length 1309;
Best Local Similarity 23.3%; Pred. No. 25;
Matches 38; Conservative 17; Mismatches 51; Indels 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 C -> S (IN REF. 3).
148413 MW; 6B77D39A95021F84 CRC64;
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-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: Contains 1 BRCT domain.
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EMBL; Z48612; CAA88497.1; -.
PIR; S59424; BV3YD9.
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PDB, IFHR, 16
PDB, 1J441, 00
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1 DIVPDNHRNKFKVINVDDDG......NNHQTELEVPRIPRIPG 130
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries
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1: sp archea:*
2: sp bacteria:*
3: sp fungi:*
4: sp human:*
5: sp_invertebrate:*
6: sp_ammal:*
7: sp_mhc:*
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sp_virus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q8wu20 homo sapien	Q8c180 mus musculu	Q90zf5 xenopus lae	Q7zwm2 xenopus lae	Q8uvu3 xenopus lae	043559 homo sapien		044830 caenorhabdi	Q9v114 drosophila	Q8mt60 drosophila	Q9qzk7 mus musculu	Q8wuz8 homo sapien	homo	Q96hi2 homo sapien	Q8n5a4 homo sapien	Q9w3r6 drosophila
SUMMARIES	ID	Q8WU20	Q8C180	Q90ZF5	Q7ZWM2	Q8UVU3	043559	Q91WJ0	044830	Q9VLL4	QBMT60	Q9QZK7	QBWUZ8	Q96LU2	Q96HI2	Q8N5A4	Q9W3R6
	DB	4	11	13	13	13	4	11	Ŋ	Ŋ	Ŋ	11	4.	4	4	4	Ŋ
	Query Match Length DB	512	508	509	509	509	492	492	195	442	442	444	223	223	257	412	622
æ	Query	100.0	98.4	88.6	88.6	88.1	73.3	9.69	25.6	25.0	25.0	20.3	19.8	19.8	19.8	19.4	19.3
	Score	969	685	616.5	616.5	613.5	510.5	484.5	178	174	174	141	137.5	137.5	137.5	135	134.5
	Result No.		7	æ	4	ഗ	9	7	œ	σι	10	11	12	13	14	15	16

Omot	Q8tew6 homo sapien	OMOC	Omo	Q8bri3 mus musculu	Q99ke3 mus musculu	Q9h666 homo sapien	Q7zxt9 xenopus lae	Q8i389 plasmodium	Q9lu94 arabidopsis		Q9v191 drosophila		Q7z5v1 homo sapien	Q9u3b6 caenorhabdi	Q869q5 dictyosteli	Q7vhx6 helicobacte	Q28224 cercopithec	Q8ifp4 plasmodium	Q9gr96 leucophaea	Q9fiq7 arabidopsis	Q7vbx2 prochloroco	Q9aqf3 clostridium	Q9m006 arabidopsis	5 arak	homo		рошо	Q9mzu5 sus scrofa	
075209	Q8TEW6	Q9BTP2	Q9NVV3	Q8BRI3	Q99KE3	999н60	Q7ZXT9	Q81389	Q9LU94	Q8C8U7	Q9VL91	044122	Q7Z5V1	09изве	086905	Q7VHX6	028224	Q8IFP4	Q9GR96	Q9FIQ7	Q7VBX2	Q9AQF3	900M60	Q9C7W5	Q8NDL1	Q9H0F1	075183	Q9MZU5	
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311	326	326	326	306	325	496	320	1807	598	570	777	777	393	549	1837	475	1251	4261	1913	431	507	914	320	753	1025	1114	1354	537	
17.9	17.9	17.9	17.9	17.5	17.3	17.3	16.4	12.2	12.1	11.9	11.6	11.6	11.4	11.4	11.4	11.3	11.2	11.1	11.0	10.9	10.9	10.9	10.8	10.8	10.8		10.8	10.8	
124.5	124.5	124.5	124.5	121.5	120.5	120.5	114	85		83	80.5	80.5	79.5	79	79	78.5	78	77	76.5	76	76	76	75.5	75.5	75.5	75.5	75.5	75	
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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Q902F5;
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2003 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                           Matches 127; Conservative
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Matches 117; Conservative
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                                                                                                                                                                                                                                                                                                                                                    RTPRTPTTPG 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8355;
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SEQUENCE FROM N.A.

STRAIN-C57BL/6; TISSUB-Brain,

MEDLINE=238825; PubMed=1247,932;

MEDLINE=238825; PubMed=1247,932;

A Straubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A Straubberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Alschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bahat N.K.,

A Alschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bahat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Former A.A., Rubin G.M., Hong L.,

B Computein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,

B Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Willalon D.K., Marny D.M., Sodergren B.J., Lu X., Glibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfaud G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                           LESFESGRRCOTGOGIFAFKCARAEELFNMLQEIMQNNSINVVEEPVVERNNHQTELEVP 120
                                                                                                                                              71 LFSFESGRRCQTGQGIFAFKCARAEELFNMLQEIMQNNSINVVEEPVVERNNHQTELEVP 130
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MEDLINE=22536883; PubMed=12466851;
The FANTOM Consortium.
The RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                   DIVPDNHRNKEKVINVDDGNELGSGIMELTDTELILYTRKRDSVKWHYLCLRRYGYDSN
                                                               1 DIVPDNHRNKFKVINVDDDGNELGSGIMELTDTELILYTRKRDSVKWHYLCLRRYGYDSN
                                 Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI TaxID=10090;
                                 .
0
 Length 512;
                               0; Indels
                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
SUC1-associated neurotrophic factor target (Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
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100.0%; Score 696; DB 4;
100.0%; Pred. No. 4.5e-68;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                    508 AA.
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STRAIN=C57BL/6; TISSUE=Brain;
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                Best Local Similarity 100.
Matches 130; Conservative
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131 RTPRTPTTPG 140
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"Xenopus FRS2 is involved in early embryogenesis in cooperation with
the Src family kinase Laloo.";
EMBO Reports 0.0-012001).
EMBL, AB064525; BAB61837.1;
GO; GO:0005158; F:insulin receptor binding; IEA.
InterPro; IPR002404; InSln_receptor51.
SMART; SM00310; PTB1; 1.
                                                                                                                                                                                                                                                                                                                                                Gaps
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                                                                     Length 508;
                                                                                                                                                                                                                                                                                                                                                0; Indels
EMBL; AK028813; BAC26132.1; -.
EMBL; BC043109; AAH43109.1; -.
EMBL; BC055314; AAH55314.1; -.
GO; GO:0005158; F:insulin receptor binding; IEA.
InterPro; IPR002404; Insln_receptorS1.
FFam; PF02174; IRS; 1.
SWART; SW00310; PTBI; 1.
Hypothetical protein.
SEQUENCE 508 AA; 56794 MW; DFFEBABIBBFFB631 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                        Score 685; DB 11;
Pred. No. 7.3e-67;
3; Mismatches 0;
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71 LFSFESGRRCQTGQGIFAFKCARAEELFNMLQEIMQNNTISVVEEPVVER-NPQTELDVP 129
                                                               LFSFESGRRCQTGQGIFAFKCARAEELFNMLQEIMQNNSINVVEEPVVERNNHQTELEVP 120
Xu H., Lee K.W., Goldfarb M.;
"Novel recognition motif on fibroblast growth factor receptor mediates direct association and activation of SNT adapter proteins.";
J. Biol. Chem. 273:17987-17990(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OTT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to sucl. associated neurotrophic factor target 2 (FGFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 492;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Straubberg R.; Straubberg R.; Straubberg R.; Straubberg R.; Submitted (dUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF005(118, AAB92555.1; -
EMBL; BC010611; AAH10611.1; -
Genew; HGNC:16970; FR83
GO; GO:0007165; P:FGF receptor signaling pathway; TAS.
GO; GO:0007165; P:Signal transduction; TAS.
InterPro; IFR00244; Insln_receptorSl.
FFGAT; SR010310; PTBI; 1.
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Last annotation update)
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MEDLINE=98324992; PubMed=9660748;
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Matches 92; Conservative
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CTT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to sucl-associated neurotrophic factor target (FGFR signalling
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Akagi K., Mood K., Daar I.O.;
"Fibroblast Growth Factor Receptor-Induced Mesoderm Formation in Xenopus Embryos Is Mediated by Adaptor Protein SNT.";
Submitted (JUTV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF390895; AAL57304.1; -.
GO; GO:0005158; F:insulin receptor binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.1%; Score 613.5; DB 13; Length 509; 88.5%; Pred. No. 5.7e-59; ive 10; Mismatches 4; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13; Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 616.5; DB 13; Leusum
Pred. No. 2.7e-59;
.....t-hes 5; Indels
                                                                                                                                                                                                                                                                                                                       Klein S., Strausberg R.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BCO46943, AA446943.1; -.
GO, GO:0005158; F:insulin receptor binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                509 AA; 56965 MW; 7FB6CEA4DCD6DF5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002404; Insln_receptorSl.
Pfam; PF02174; IRS; 1.
SMART; SM00310; PTBT; 1.
SEQUENCE 509 AA; 56923 MW; 8F8E724A01CA3847 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Suc1-associated neurotrophic factor target XSNT.
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               AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Mismatches
             509
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Pfam; PF02174; IRS; 1.
SMART; SM00310; PTBI; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                          Kenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 90.0
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                                                                                                                                                                                                                  Xenopodinae; Xenopus
NCBI_TaxID=8355;
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TISSUE=Embryo;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                         adaptor)
               Q7ZWM2
Q7ZWM2;
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Shownkeen R.,

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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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                                                                                                                                                                                 Nature 368:32-38(1994).
                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-Bristol N2;
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STRAIN=Berkeley;
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Q9VLL4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 LFSFESGRRCQTGQGGFPAFKCSRAEDIFNLLQDLMQCNSINVTEEPVIITRSSHPPELDL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DTVPDNHRNKFKVINVDDDGNELGSGIMELTDTELILYTRKRDSVKWHYLCLRRYGYDSN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 DSVPHNHPTKFKVTNVDDEGVELGSGVMELTQSELVLHLHQREAVR#PYLCLRRYGYDSN 70
                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhou L., McDougall K., Kubu C.J., Verdi J.M., Meakin S.O.,
"Genomic Organization and Comparative Sequence analysis of the Mouse
and Human FRS2, FRS3 genes.";
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC014819; AAH14819; 1; -.
EMBL; AF556480; AAO15529.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Bristol N2;
MEDINE=94180718; PubMed=7906398;
Milson R., Anderson K., Baynes C., Berks M.,
Wilson R., Bustron J., Cornell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Laiteille P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda, Chromadorea, Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                           Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
signalling adaptor) (Fibroblast growth factor receptor substrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.6%; Score 484.5; DB 11; Length 492; 69.3%; Pred. No. 9.3e-45; Live 21; Mismatches 17; Indels 1;
                                                                                                                                                                                                                                                                 TISSUE=Eye, and Retina;
Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         492 AA; 53976 MW; COA895B9173394E6 CRC64;
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Last annotation update)
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InterPro; IPR002404; Insln_receptorS1.
Pfam; PF02174; IRS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00310; PTB1; 1.
PROSITE; PS00086; CYTCCHROME_P450; 1.
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06,
25,
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nes 88; Conservative
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01-JUN-1998 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
F54D12.6 protein.
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                                                     SNT2 OR FRS3.
Mus musculus (Mouse).
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                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                 NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=129/SvJ;
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66 SGRRCQTGQGIFAFKCARAEELFNMLQEIMQNNSINVVEEPVVERN-NHQTELEVPRTPR 124
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MEDLINE-20196006; PubMed=10731132;
Madams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Manatides P.G., Scherer S.E., In P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
M. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Man X.H., Doyle C., Baxter E.G., Halt G., Nakson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basua A., Baxendale U., Bayartaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolahakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
A Burtis K.C., Busam D.A., Butler H., Caddeu E., Center A., Chandra I.,
A Cherry J.M., Cawley S., Dahlke C., Davenmour L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 HGNRKK-----NBLVHAWLRVTRTTITLEISKKECLVWPLPLIRRYGYTSAGIFFFE 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Gaps
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkee Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Waterstock L., Wilkinson-Sproat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Bukaryota, Brdopterygota, Diptera, Brachycera; Muscomorpha,
Bphydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 195;
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25.6%; Score 178; DB 5; Length 19;
Best Local Similarity 32.5%; Pred. No. 1.9e-11;
Matches 39; Conservative 30; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston R.;
submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF040647; AAB94991.1;
PIR; T32819; T32819
Wormbep; F54012.6; CE17871.
GO; GO:0005158; F:insulin receptor binding; IEA.
InterPro; IPR002404; Insln_receptorS1.
InterPro; IPR00408; Reg_chr_condens.
                                                                                                                                                                                                                                                                                                                                                                                                                Maggi L., Goela D.;
"The sequence of C. elegans cosmid F54D12.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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(JUN-2002) to the EMBL/GenBank/DDBJ databases
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             Submitted
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Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann M.,

Glodek A., Gang Fl., Garg N.S., Gelbart W.M., Glasser K.,

A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

Harris N.L., Harvey D., Heinan T.J., Hernandez J.R., Houck J.,

A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

R. Mishina D., Houston K.A., Li J., Wei M.-H., Ibegwam C.,

R. Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

R. Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

R. Martei B., McIntosh T.C., Morris J., Moshrefi A.,

Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

R. Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

R. Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

Spier B., Schafling A.C., Staplecon M., Strong R., Smith T.,

Spier B., Spradling A.C., Staplecon M., Strong R., Smith T.,

Mulliams S.M., Woodage T., Weinstock G.M., Weissenbach J.,

R. A. Long F.N., Weinstock G.M., Weissenbach J.,

A. Lang X.H., Zhong F.N., Reining W., Zhou X., Zhu S., Zhu X., Smith H.O.,

R. Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.,

R. Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.,

R. The genome sequence of Drosophila melanogaster.",

R. Smith H.O.,

R. Schielez S.N., Rocheller B., Wenter J.C.,

R. Schielez S.N., Rocheller B., Smith H.O.,

R. Schence Z.SISISISS-SISISISSON.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPEAGRRCMSGPGIYTFRVHNAEQLYPMFQRYINAVNTDAFVQGERERVNSAHSVSVNMG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 HRNKFKY----INVDDDGNELGSGIMELTDTELILYTRKRDSVKWHYLCLRRYGYDSNLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Eachycera, Muscomorpha, Ephydroida, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.0%; Score 174; DB 5; Length 442; 34.4%; Pred. No. 1.5e-10;
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Last annotation update)
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FlyBase, FBGH0032042, CG13398.
GO; GO:0005158; F:insulin receptor binding; IEA.
InterPro; JFR002404; Insln_receptorS1.
PFan; PF02174; IES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Pred. No. 1.5e
22; Mismatches
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01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42; Conservative
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                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                 LGSGIMELTDTELILYTRKRDSVKWHYLCLRRYGYDSNLFSFESGRRCQTGQGIFAFKCA
                                                                                                                                                                                                                                                        7 HRNKFKV----INVDDDGNELGSGIMELTDTELILYTRKRDSVKWHYLCLRRYGYDSNLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cong F., Yuan B., Goff S.P.; "Characterization of a Novel Member of the DOK Family that Binds and Modulates Abl Signaling.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lemay S., Davidson D., Latour S., Veillette A., "Dok-3, a novel adapter molecule involved in the negative regulation
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                               52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of immunoreceptor signaling.";
Mol. Cell. Biol. 20:2743-274(2000).
EMBL, AF179942; AAF14285.1;
EMBL, AF23780; AAF61309.1;
GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0005115; F:protein binding; IPI.
GO; GO:0007265; P:RAS protein signal transduction; IDA.
InterPro; IPR001849; PH.
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                                                                                                       I; 1.
48217 MW; FD67D8BE3A5BF038 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Adaptor protein (Inhibitory adapter molecule DOK3).
DOKI OR DOK3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.3%; Score 141; DB 11; I 28.3%; Pred. No. 6.5e-07; ive 20; Mismatches 47;
EMBL, AY118363, AAM48392.1, -.
FlyBase, FBgn0032042, CG13398.
GO; GO:0005158, F:insulin receptor binding; IEA.
                                                                                                                                                                     Score 174; DB 5;
Pred. No. 1.5e-10;
                                                                                                                                                                                     34.4%; Pred. No. -
                                                                InterPro; IPR002404; Insln_receptorS1
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                                                                                                                                                                     25.0%;
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les 36; Conservative
                                                                                                                                                            Query Match
Best Local Similarity 34.44
Marches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00233; PH; 1.
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Pfam; PF00169; PH; 1.
                                                                                Pfam; PF02174; IRS; 1.
SMART; SM00310; PTBI;
SEQUENCE 442 AA; 48
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[1]
SEQUENCE FROM N.A.
TISSUE=Brain;
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RAPDICGVVAAAIARQRERLPELAMSPPCPLPRALSLPSLEPPGELREVAPGFELPTRK 298
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                                                                  -----EPVVERNNHQTELEVPRTPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 CARAEELFNMLQEIMQNNSINVVEE-----PVVERNNHQTELEVPRT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRECE----MIYOXVHSATLAIAEQHERLMLEMEQKARLQTSLTEPMT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Straubers, Straubers, Straubers, Straubers, Straubers, Straubers, Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL, BCO19045; AAH19045.1; -- GO, GO:0005158; F:insulin receptor binding; IEA. InterPro; IPRO03404; Insln_receptorS1. Pfam; PF02174; IRS; 1. SMART; SM00310; PTBI; 1. Hypothetical protein. SEQUENCE 223 AA; 25538 MW; DFD6F27B1981AEBB CRC64;
                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ25066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
19.8%; Score 137.5; DB 4;
Best Local Similarity 31.5%; Pred. No. 6.8e-07;
Matches 34; Conservative 19; Mismatches 42;
                                                                                                                                                                                                                                                                                                        223 AA.
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                                                                  RABELFINMLQEIMQNNSINVVE----
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                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                    125 TP-TTPG 130
                                                                                                                                                                                           299 LPLTDPG 305
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                                                                                                                                                                                                                                                      RESULT 12
28WUZ8
AC Q8WUZ8,
DT 01-MAR.
DT 01-MAR.
DE HYPOTHER
OC MAMMAILTA.
RN [1] TASUBER
RP SEQUENCY
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                                                                                                                                                                                                                                                                          24 GSGIMELIDIELILYTRKRDSVK---WHYLCLRRYGYDSNLFSFESGRRCQTGQGIFAFK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 GSGIMELTDTELILYTRKRDSVK---WHYLCLRRYGYDSNLFSFESGRRCQTGQGIFAFK 80
                                                                                                                                                                                                                          13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                             19.8%; Score 137.5; DB 4; Length 223; 31.5%; Pred. No. 6.8e-07; tive 19; Mismatches 42; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                       105 TREGE----MIYQKVHSATLAIAEQHERLVLEMEQKARLQTSLTEPMT 148
                                                                                                                                                                                                                                                                                                                                                                                  81 CARABELFNMLQEIMQNNSINVVEE-----PVVERNNHQTELEVPRT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.8%; Score 137.5; DB 4; Length 257; 31.5%; Pred. No. 8.1e-07; Live 19; Mismatches 42; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 CARAEELFUMLQEIMQNNSINVVEE-----PVVERNNHQTELEVPRT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
BMBL, BC008583, AAH08583.1, -,
GO, GO:0005159; Finsulin receptor binding; IBA.
InterPro; IPR002404; Insln_receptorS1.
Pfam; PF02174; IRS; 1.
Pfam; PF02174; IRS; 1.
Hypothetical protein.
In InterPro; IPR0310; IPR1; 1.
InterPro, IPR002404; Insln_receptorS1.
Pfam; PF02174; IRS; 1.
SWART; SM00310, PTBI; 1.
Hypothetical protein.
SEQUENCE 223 AA; 25506 WW; 2B87B77A499B05A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 257 AA; 29455 MW; 931D34A8F12A952A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q96H12;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DCT-2003 (TrEMBLrel. 25, Last annotation.update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                 Query Match
Best Local Similarity 31.5°,
10.00 34; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2003 (TrEMBLrel. 25, Docking protein 2, 56kD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Search completed: August 2, 2004, 09:31:15 Job time: 60.1579 secs

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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                    US-08-980-523-9
                                         Sequence 9, Appli
Sequence 11, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 1, Appli
Sequence 10, Appli
Sequence 9, Appli
Sequence 44, Appli
Sequence 4481, Appli
Sequence 5131, Appli
Sequence 23, Appli
Sequence 23, Appli
Sequence 23, Appli
Sequence 23, Appli
Sequence 24, Appli
Sequence 5, Appli
Sequence 64, Appli
Sequence 64, Appli
Sequence 64, Appli
Sequence 448, Appli
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Sequence 125, App
Sequence 5487, Ap
                                                                                  August 2, 2004, 09:27:44; Search time 24.8026 Seconds (without alignments) 270.591 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                              696
1 DIVPDNHRNKFKVINVDDDG......NNHQTELEVPRIPRIPG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                             Issued Patents AA.*
1: /cgm2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgm2_6/ptodata/2/iaa/5B_COMB.pep:*
4: /cgm2_6/ptodata/2/iaa/6A_COMB.pep:*
5: /cgm2_6/ptodata/2/iaa/RB_COMB.pep:*
6: /cgm2_6/ptodata/2/iaa/PCTUS COMB.pep:*
6: /cgm2_6/ptodata/2/iaa/PCTUS COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-980-523-9
US-08-980-523-11
US-08-980-523-11
US-08-980-523-11
US-08-317-310A-15
US-08-317-310A-15
US-08-51-13
US-08-51-13
US-08-51-13
US-08-51-13
US-08-51-13
US-08-51-13
US-08-51-13
US-08-61-13
US-09-489-647-132
US-09-489-647-23
US-09-489-647-23
US-09-489-647-23
US-09-508-691-5131
US-09-508-691-5131
US-09-508-691-6491
US-09-134-001C-4435
US-09-134-001C-5887
                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                389414 segs, 51625971 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                US-09-757-415A-1_COPY_11_140
                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       using sw model
                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
                                                         - protein search,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.5
66.5
65.5
65.5
65
                                                                                                                                               Title:
Perfect score:
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679
143.5
78
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                                                           OM protein
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                                                                                                                                                                                                                                                     Searched:
                                                                                        Run on:
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No.
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ALIGNMEN

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US-08-806-523-9

US-08-806-523-9

Parent No. 6310181

CAREAL INFORMATION:

APPLICANT: Spivak-Kroizman, Taly
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION:

CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: 613 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
COMPUTES: Beatego for Windows 2.0
CITY: 100 MAPPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: PastERM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Reatego for Windows 2.0
CURRENT REPLICATION NUMBER: US/08/990,523
FILING DATE: December 1, 1997
CLASSIFICATION NUMBER: 60/032,033
FILING DATE: December 1, 1997
APPLICATION NUMBER: 60/032,033
FILING DATE: December 1, 1997
APPLICATION NUMBER: 32,327
TELEFAM: (213) 955-0440
TELEFAM: (213) 955-0440
TELEFAM: 67-3510
TELEFAM: 67-3510
TELEFAM: 67-3510
TELEFAM: 67-3510
TELEFAM: 67-3510
TELEFAM: STREET SIGNAL STREET
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61 LFSFESGRRCQTGQGIFAFKCARABELFNMLQEIMQNNSINVVEEPVVERNNHQTELEVP 120
                                                                                                                                                                 61 LFSFESGRRCQTGQGIFAFKCARAEELFNMLQEIMQNNSINVVEEPVVERSSHQTELEVP 120
                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Carpino, Nicholas A.
APPLICANT: Kobayashi, Ryuji
APPLICANT: Kobayashi, Ryuji
APPLICANT: Mishishewski, David G.
APPLICANT: Strife, Annabel O'C.
APPLICANT: Clarkson, Bayard D.
ITLE OF INVENTION: A No. 6100386el Human Gene/Protein Involved in TITLE OF INVENTION: A No. 6100386el Human Gene/Protein Involved in TITLE OF INVENTION: A No. 6100386el Human Gene/Protein Involved in CRRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
                                                                           1 DIVPDNHRNKFKVINVDDDGNELGSGVMELTDTELLILYTRKRDSVKWHYLCLRRYGYDSN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 GSGIMELTDTELILYTRKRDS-----VKWHYLCLRRYGYDSNLFSFESGRRCQTGQGIF 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 AFKCARAEELFNMLQEIMQNNSINVVE---EPVVERNNHQTELEVPRTPRTP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 481;
    0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/787,091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 20.6%; Score 143.5; DB 3; Best Local Similarity 29.5%; Pred. No. 2.6e-09; Matches 33; Conservative 20; Mismatches 50;
    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,418
FILING DATE: U. NOV 1996
ATTORNEY/AGENT INTORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL96-05PA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            US-08-787-091-2; Sequence 2, Application US/08787091; Patent No. 6100386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 481 amino acids amino acid
    Matches 126; Conservative
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MOLECULE TYPE: protein
US-08-787-091-2
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                                                                                                                                                                                                                                                                       121 RTPRTPTTP 129
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                                                                                                                                    1 DTVPDNHRNKFKVINVDDDGNELGSGIMELTDTELILYTRKRDSVKWHYLCLRRYGYDSN 60
                                                                                                                                                              11 DIVPDNHRNKFKVINVDDDGNELGSGVMELIDTELILYTRKRDSVKMHYLCLRRYGYDSN
                                                                                          0; Gaps
                                          Length 508;
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                                             Score 685; DB 4; Length 50:
Pred. No. 4.4e-77;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kouhara, Haruhiko
APPLICANT: Spivak-Kroizman, Taly
APPLICANT: Spivak-Kroizman, Taly
APPLICANT: Lax, Irit
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon F. T.
STRPFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 679; DB 4;
Pred, No. 3.6e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FESSERG COF WAINDOWS 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/980,523
FILING DATE: December 1, 1997
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US97/21851
FILING DATE: December 1, 1997
APPLICATION NUMBER: 60/032,093
FILING DATE: December 3, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 90071-2066
COMPUTER READBLE FORM:
MEDIUM TYPE: 55" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 230/045
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/08980523
Patent No. 6310181
GENERAL INFORMATION:
APPLICANT: Kouhara, Haruhiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                          Query Match
Best Local Similarity 97.7%;
Matches 127; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.6%;
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                                                                                                                                                                                                                                                                                                                  121 RIPRIPITPG 130
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; MOLECULE TYPE: protein
US-08-980-523-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Los Angeles
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: sin
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Best Local Similarity
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US-08-980-523-9
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232 TPOTAQGNDIFQAVETAIHRQKAQGKAGQGHDVLRADSHEGEVAEGKLPSPP 283

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Sequence 1, Application US/09508691
; Sequence 1, Application US/09508691
; Patent No. 6498139
; GENERAL INFORMATION:
APPLICANT: YASAKI, YOSHIO
; APPLICANT: KABA, AKIRA
TITLE OF INVENTION: REMEDIES FOR DISEASES CAUSED BY INSULIN RESISTANCE
FILE REFERENCE: 4895-0019-0PCT
CURRENT APPLICATION NUMBER: US/09/508,691
CURRENT PILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US/09/25
; PRIOR PLILING DATE: 1998-09-25
; PRIOR FILING DATE: 1998-09-25
; PRIOR FILING DATE: 1997-09-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PATENTIN VETSION 3.0
; SEQ ID NOS: 5
; FEATON NOTES OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----VDDSVVAQN 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52 LRRYGYDSNLFSFESGRRCQTGQGIFAFKCARAEELFNMLQEIMQNNSINVVEEPVVERN 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.2%; Score 78; DB 4; Length 1242; 30.0%; Pred. No. 1.6; tive 7; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 11.2%; Score 78; DB 5; Length 1234; Best Local Similarity 30.0%; Pred. No. 1.6; Matches 21; Conservative 7; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 IRRCGHSENFFFIEVGRSAVTGPGEFWMQ----
MEDIUM TYPER LEFTORY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13041
FILING DATE: Herewith
FILING DATE: Herewith
RICH APPLICATION NUMBER: 98/317,310
FILING DATE: 03-00T-1994
ATTORNEY/AGENT INFORMATION:
RAFERENCE/DOCKET NUMBER: 35,965
REFERENCE/DOCKET NUMBER: JDP-022PC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1234 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 30.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 MHETILEAMR 253
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US95-13041-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----VDDSVVAQN 243
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Sequence 15. Application PC/TUS9513041
GENERAL INFORMATION:
APPLICANT: WHITE, Morris F.
APPLICANT: BIRNE, Jacalyn H.
TITLE OF INVENTION: THE IRS FAMILY OF GENES
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
                                                                                                                                                                                        APPLICANT: WHITE, Morris F.
APPLICANT: SUN, Xiao Jian
APPLICANT: SUN, Xiao Jian
APPLICANT: PIERCE, Jacalyn H.
TITLE OF INVENTION: THE IRS FAMILY OF GENES
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: MASSACHIBECUS
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,310A
FILING DATE: 03-0CT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LOUIS MYGETS
REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: JDP-022
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1234 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1: 1234 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 30.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 NHQTELEVPR 121
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.52 LRRYGYDSNLFSFESGRRCQTGQGIFAFKCARAEELFNMLQEIMQNNSINVVEEPVVERN 111
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Fatent NO. 582730
GENERAL INFORMATION:
FAPPLICANT: Pedersen, Oluf
APPLICANT: Frederiksen, Kathrine A.
TITLE OF INVENTION: WURSTRATE 1
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 58277300 NO. 5827730th America
STREET: 405 Lexington Avenue
COUNTRY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
11.2%; Score 78; DB 2; Length 1243;
Best Local Similarity 30.0%; Pred. No. 1.6;
Matches 21; Conservative 7; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: User.

ZIP: 10174

COMPUTER READABLE FORM:
MEDDIUM TYPE: Floppy disk
COMPUTER IBM PC compatible
COMPUTER: IBM PC compatible
COMPAND: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/557,139
FILING DATE: 12-FEB-1996
CLASSIFICATION: 800
ATTORNEY/ACENT INFORMATION:
NAME: Lambiris: Elias J
REGISTRATION NUMBER: 4041.204-US
REPERBNCS/DOCKET NUMBER: 4041.204-US
TELEPAX: (212) 867-0123
INFORMATION EN SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1243 amino acids
TENGTH: Liba amino acids
TENGTH: Liba amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/08980523
| Patent No. 6310181
| GENERAL INFORMATION:
| APPLICANT: Kouhara, Haruhiko
| APPLICANT: Spivak-Kroizman, Taly
| APPLICANT: Spivak-Kroizman, Taly
| APPLICANT: Schlessinger, Joseph
| TITLE OF INVENTION: ADAPTOR PROTEIN FRS2 AND
| TITLE OF SEQUENCES: 11
| CORRESPONDENCE ADDRESS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-557-139-2
                                 112 NHQTELEVPR 121
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PRESENCE INCOME & John Street
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LOCATION: (414)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE
COCATION: (189)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids FRATURE:
DOCATION: SITE
LOCATION: (275)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids other INFORMATION: (275)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                           97 PKLINRENFPGVSWDSLPDELLLGIFSCLCLPELLKVSGVCKRWYRLASDESLWQTLDLT- 155
                                                                                                                                                                                                                                                                                       4 PDNHRNKFKVINVDDDGNELGSGIME-LIDIELI-----LYTRKRDSVKWHYLCLRR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                   55 YGYDSNLFSFESGRRCQTGQGIFAFKCARA--------EELFNMLOEI--- 94
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                   48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 HGILSQCSKLQNLSLELRLSDPIVNTLAKNSNLVRLNLPGCFGFFKFP 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 ------MONNSINV-VEEPVVE---RNNHQTELEVPRTPRTPTTP 129
                                                                                                                                       Length 435;
                                                                                                                                                                                                                   58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-99-489-847-1122
Sequence 132, Application US/09489847
Patent No. 6476195
GENERAL INFORMATION
APPLICANT: Rosen et al
TITLE OF INVENTION: 98 Human Secreted Froteins
TITLE OF INVENTION: 98 Human Secreted Froteins
FILE REPERENCE: PS031P1
CURRENT APPLICATION NUMBER: US/09/489,847
CURRENT FILING DATE: 2000-01-24
CURRENT FILING DATE: 1999-07-29
EARLIER PELING DATE: 1999-07-29
EARLIER PILING DATE: 1999-07-29
EARLIER PILING DATE: 1999-06-5
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-05
EARLIER FILING DATE: 1998-08-06
EARLIER PILING UNCS: 376

SEQ ID NO 132
LIENGTH: 709
                                                                                                                                                   Ouery Match

10.8%; Score 75; DB 2;
Best Local Similarity 23.8%; Pred. No. 0.87;
Matches 40; Conservative 22; Mismatches

Matches 40; Conservative 22; Mismatches
           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-531-439B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: SITE
LOCATION: (438)
OTHER INFORMATION: X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAMĖ/KEÝ: SITE
LOCATION: (641)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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Sequence 4, Application US/08531439B

Patent NO. 5981702

GENERAL INFORMATION:
APPLICANT: Zhang, Hui
APPLICANT: Zhang, Hui
APPLICANT: Zhang, Hui
APPLICANT: Aboutd
TITLE OF INVENTION: O'Cyclin/CDK Associated Proteins,
TITLE OF INVENTION: and Uses Related Thereto
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley, Hoag & Eliot
STAEET: One Post Office Square
CITY: Boston
STATE: MA
COUNTY: USA
COMPUTE: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 11.1%; Score 77; DB 3; Length 38; Best Local Similarity 40.6%; Pred. No. 0.016; Matches 13; Conservative 9; Mismatches 10; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rclease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,091
FILING DATE:
CLASSIFICATION TOWNER: US 60/030,418
PILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: GEARANAN PRETICIA
REFERENCE/POCKET NUMBER: 32,227
REGISTRATION NUMBER: 32,227
REFERENCE/POCKET NUMBER: 32,227
REFERENCE/POCKET NUMBER: 32,227
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: 617-661-6240
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LESFESGRRCQTGQGIFAFKCARAEELFNMLQ 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-787-091-9
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STRANDEDNESS: not
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RESULT 14
US-08-894-017-23
Sequence 23, Application US/08894017
Patent No. 6024958
GENERAL INFORMATION:
APPLICANT: Lehner, Thomas
APPLICANT: Lehner, Thomas
TITLE OF INVENTION: POLYPEPTIDE FRAGMENTS CAPABLE
TITLE OF INVENTION: OF_COMPETITION WITH STREPTOCOCCUS MUTANS ANTIGEN I/II
                                                                                                                                                                                                                                                                                                                                     47 WHYLCLRRYGYDSNLFSFESGRRCQTGQGIFAF----KCARABELFNMLQEIMQNNSIN 101
                                                                                                                                                                                                          2 TVPDN-----HRNKFKVINVDDDGNELGSGIMELT-----DTELILYTRKRDSVK 46
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                                                                                                                                                           Gaps
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                                                                                                                                                                23;
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                                                                                                                DB 4; Length 342;
                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: MORRISON & FOERSTER
2000 Pennsylvania Avenue, NW, suite 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastEBM: Windows
SOFTWARE: FastEBM: Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,017
FILING DATE: 31-UTL-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/GB96/00207
FILING DATE: 31-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Murashioe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28;
                                                                                                                                                                46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.8%; Score 68.5; DB 3;
20.4%; Pred. No. 34;
tive 18; Mismatches 58;
                                                                                                                Query Match
9.8%; Score 68.5; DE
Best Local Similarity 20.5%; Pred. No. 4;
Matches 25; Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 25150-20067.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-822-0168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 VPDNHRNKFKVINVDDDGNELG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 23
SEQUENCE CHARACTERISTICS:
LENGTH: 1561 amino acids
                         TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2'
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 31; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: si
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310 VI 311
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                                                    ; OKGANISM: FIOUEI
US-09-543-681A-5131
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STREET: 20
LENGIH: 342
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BENERAL INFORMATION:
APPLICANT: LYAND DOUGETE-Stamm et al
APPLICANT: LYAND DOUGETE-Stamm et al
APPLICANT: LYAND DOUGETE-Stamm et al
APPLICANT: LYAND DOUGETE ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/9/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674

LENGTH: 541
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Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
NUMBER OF SEQ ID NOS: 8344
               NAME/KEY: SITE LOCATION: (696) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                    ; LOCATION: (697)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-489-847-132
                                                                                                                                                                                                                                                                                                                                                                     545 GVFTVTPDTKSKVYLRTPNWDRGLPSLTSVSWNISVPRDQVACLIFFKERSGVVCQTGRA 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 DVVVHILDEKGĞPDFVFVREKYSDSLMKLLS--LVSTPYNTVIDNEYWDNQYQQDKTIQR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----COTGOGIFAFKCAR-AEELFNMLQEIMQNNSINVVEEPVVERNNHQTELEVPR 121
                                                                                                                                                                                                                                                                                                                           26 GIMELT-DTELILYTRKRD-----SVKWHYLCLRRYGYDSNLFSFESGRRCQTGQG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 --IFAFKCARAEELFNMLQEIMQNNS-----INVVEEPVVERNNHQTELEVPRTPRT 125
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                                                                                                                                                                                                                            10.7%; Score 74.5; DB 4; Length 709;
25.2%; Pred. No. 2;
tive 17; Mismatches 53; Indels 19; Gaps
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Best Local Similaritý 25.8%; Pred. No. 2.4;
Matches 31; Conservative 21; Mismatches 37; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4481, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Staphylococcus epidermidis US-09-134-001C-4481
                                                                                                                                                                                                                            Query Match
Best Local Similarity 25.2%
Matches 30; Conservative
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                                                                                       FEATURE:
NAME/KEY: SITE
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| Sequence 23, Application US/09456474
| Sequence 23, Application US/09456474
| Patent No. 6500433
| GENERAL INFORMATION:
| APPLICANT: Lehner, Thomas
| APPLICANT: Lehner, Thomas
| TITLE OF INVENTION: COMPETITION WITH STREPTOCOCCUS MUTANS ANTIGEN |
| FILE REPRENCE: 2515-2067.10
| CURRENT PILING-DATE: 1999-12-09
| PRIOR PILING-DATE: 1999-12-09
| PRIOR PILING DATE: 1997-10-20
| NUMBER OF SEQ ID NOS: 29
| NUMBER OF SEQ ID NOS: 29
| NUMBER OF SEQ ID NOS: 29
| SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                      39 -IRKRDSVKWHYLCLRRYGYDSNLFSFESGRRCQTGQGIFAFKCARAEELFNMLQEIMQN 97
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9.8%; Score 68.5; DB 4; Length 1561;
Best Local Similarity 20.4%; Pred. No. 34;
Matches 31; Conservative 18; Mismatches 58; Indels 45.
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                                                                                                                                                                                                                                                             ; SEQ ID NO 23
; LENGTH: 1561
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-09-456-474-23
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Job time : 24.8026 secs
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August 2, 2004, 09:31:19; Search time 69.2763 Seconds (without alignments) 588.640 Million cell updates/sec
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696
1 DTVPDNHRNKFKVINVDDDG......NNHQTELEVPRTPRTTPG 130
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'(cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
'(cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
'(cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
'(cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
'(cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
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'(cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1291235 segs, 313682936 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published_Applications_AA:*
                                                                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		Sequence 67, Appl	Sequence 2192, Ap	Sequence 1, Appli	Sequence 3, Appli	Sequence 179, App	Sequence 58, Appl	Sequence 6, Appli	Sequence 285, App	Sequence 6260, Ap	Sequence 33396, A	Sequence 2340, Ap	Sequence 5, Appli	Sequence 2, Appli	Sequence 3, Appli
DI	US-09-757-415A-1	US-10-146-473-67	US-10-276-774-2192	US-09-731-660A-1	US-09-731-660A-3	US-10-001-870-179	US-09-789-919-58	US-10-307-928A-6	US-10-112-944-285	US-10-106-698-6260	US-10-029-386-33396	US-10-264-049-2340	US-10-192-381-5	US-09-731-660A-2	US-10-694-874-3
	10	14	12	12	12	13	σ,	15	12	14	14	15	14	12	16
% Query Match Length DB	508	508	521	508	129	541	359	331	440	289	268	268	105	114	1231
% Query Match	100.0	100.0	100.0	98.4	97.6	20.6	20.3	19.8	17.3	16.0	13.7	13.7	11.2	11.2	11.2
Score	969	969	969	685	619	143.5	141	137.5	120.5	111.5	95.5	95.5	78	78	78
Result No.			ų	4	5	9	7	00	თ	10	11	12	13	14	15

16 78 11.2 1242 9 US-09-903-248-5 19 78 11.2 1242 9 US-09-859-604-5 19 78 11.2 1242 9 US-09-859-604-5 20 78 11.2 1242 9 US-09-903-016-5 21 78 11.2 1242 9 US-09-903-105-5 22 78 11.2 1242 9 US-09-903-105-5 23 78 11.2 1242 10 US-09-436-184-5 24 78 11.2 1242 10 US-09-436-184-5 25 78 11.2 1342 13 US-10-085-027-1 26 75 10.8 99 12 US-10-34-143-10 27 75 10.8 99 12 US-10-44-59-217303 29 74.5 10.7 520 12 US-10-47-59-217303 29 74.5 10.7 520 12 US-10-47-59-217303 29 74.5 10.7 520 12 US-10-282-122A-7487 29 74.5 10.7 520 12 US-10-282-122A-74807 29 74.5 10.7 520 12 US-10-282-122A-74637 29 74.5 10.7 520 12 US-10-282-122A-74837 29 74.5 10.7 520 12 US-10-282-122A-74837 29 74.5 10.7 520 12 US-10-282-122A-74837 29 74.5 10.7 520 12 US-10-282-122A-74537 29 72.5 10.4 437 14 US-10-156-761-12680 20 72.5 10.4 519 12 US-10-29-21237 20 72 10.3 1331 14 US-10-136-3493-1656 21 10.2 US-10-282-122A-47351 22 10.3 1330 15 US-10-282-122A-77351 24 70.5 10.1 3170 14 US-10-128-714-8504 25 70.5 10.1 3170 14 US-10-128-714-8504	Sequence 5, Appli		'n	ທີ	'n	'n	a)	_	٠,	٠.	•••	•	Sequence 71887, A	12463	Sequence 132, App	2310,	Sequence 213391,	Sequence 45402, A		Sequence 12680, A		71027	272	50, A	165	e 4735	4.	'n	4, Appl	Sequence 8504, Ap
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	11.2	11.2	11.2	11.2	11.2	11.2	11.2				10.8	10.8	10.7	10.7	10.7	10.7	10.6	10.6	10.4	10.4	10.4	10.4	10.3	10.3	10.3	10.2	10.2	•		10.1
11110000000000000000000000000000000000	78	78	78	7.8	7.8	78	78	78	78	78	75	75	74.5	74.5	74.5	74.5	74	74	72.5	72.5	72.5	72.5	72	72	71.5	\sim	71	70.5	70.5	70.5
· ·	16	17	18	19	20	21	22	23	24	25	26	27	28	53	30	31	32	33	34	35	36	3.7	38	33	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 US-09-757-4 Sequence Publication RENERAL II APPLICAN TITLE OF FILE REF CURRENT CURRENT PRIOR PIP PRIOR PIP PRIOR PIP PRIOR PIP SOFWWARE SSOFWWARE SSOFWWARE STORM PIP TYPE: PIP TYP TYP TYP TYP TYP TYP TYP TYP TYP TY	RESULT 1 US-09-75-415A-1 US-09-75-415A-1 US-09-75-415A-1 Sequence 1, Application US/09757415A Publication No. US20030040612A1 GENERAL INPORMATION: APPLICANT: Zhou, Ming-Ming TITLE OF INVENTION: Methods of Identifying Modulators of the FGF Receptor FILE REFERENCE: 2459-1-020 CURRENT APPLICATION NUMBER: US/09/757,415A CURRENT PILING DATE: 2001-01-09 PRIOR PILING DATE: 2000-01-12 NUMBER OF SEQ ID NOS: 7 SOFTWARE: Patentin version 3.1 LENGTH: 508 TYPE: PRI CURRENT Homo sapien US-09-757-415A-1
Query M Best Lo Matches	Query Match Best Local Similarity 100.0%; Score 696; DB 10; Length 508; Best Local Similarity 100.0%; Pred. No. 3.2e-73; Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
දුරු පු	1 DTVPDNHRNKFKVINVDDDGNELGSGIMELTDTELLLYTRKRDSVKMHYLCLRRYGYDSN 60
Oy Op	61 LFSFESGRRCOTGOGIFAFKCARAEELFNMLOEIMONNSINVVEEPVVERNNHQTELEVP 120
do do	121 RIPRIPITEG 130 131 RIPRIPITEG 140

RESULT 2

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Sequence 1, Application US/09721660A

Sequence 1, Application US/09721660A

Publication No. US20020086972A1

GENBRAL INFORMATION:

APPLICANT: WOURARA, HARUHIKO

APPLICANT: SOFURAR, HARUHIKO

APPLICANT: SOFURAR, TALY

APPLICANT: SOFURAR, OSEPH

TITLE OF INVENTION: ADAPTOR PROTEIN FRS2 AND RELATED PRODUCTS AND METHODS

FILE REFERENCE: 038602/1023

CURRENT PAPLICATION NUMBER: US/09/731,660A

FRIOR APPLICATION NUMBER: 08/980,523

PRIOR FILING DATE: 1995-12-01

PRIOR FILING DATE: 1996-12-03

NUMBER: OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1

LANGHIES 08

TARE DEBARMARE: DEPARTED NO 1

SEQ ID NO 1

LANGHIES 08

TARE DEBARMARE: DEPARTED NO 1

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TARE DEBARMARE: DEPARTED NO 1

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TARE DEBARMARE: DEPARTED NO 1

LANGHIES 08
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94 LFSFESGRRCQTGQGIFAFKCARAEELFNMLQEIMQNNSINVVEEPVVFRNNHQTELEVP 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 LESFESGRRCQTGQGIFAFKCARAEELFUMLQEIMQUNSINVVEEPVVERSSHQTELEVP 130
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                                                                                                                   121 RTPRTPTTPG 130
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                             RESULT 4
US-09-731-660A-1
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Sequence 2192, Application US/10276774

Publication No. US20040053245A1

SEQUENCE INFORMATION:

APPLICANT: Hyseq, Inc.

APPLICANT: Tang, Y, Tom et al

TITLE OF INVENTION: No. US20040053245A1e1 Nucleic Acids and Polypeptides

TITLE OF INVENTION: No. US20040053245A1e1 Nucleic Acids and Polypeptides

CURRENT PILING DATE: 2002-11-18

PRIOR RELING DATE: 2002-11-18

PRIOR PLING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 09/496,914

PRIOR PLING DATE: 2000-02-03

NUMBER OF SEQ ID NOS: 2700

SOFTWARE: CUSTOM

SEQ ID NO 2192

LENGTH: 521
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                            Sequence 67, Application US/10146473
Publication No. US2030108888A1
GENERAL INFORMATION.
APPLICANT: Scanlan, Matthew
APPLICANT: Scanlan, Matthew
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Gure, Ali
APPLICANT: Gure, Ali
APPLICANT: Offer, Yaon-Tseng
APPLICANT: Offer, Yaon-Tseng
APPLICANT: Old, Lloyd
TITLE OF INVENTION: Breast Cancer Antigens
FILE REFERENCE: L00461/0130 (JRV)
CURRENT PRILING DATE: 2002-05-15
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 82
SOFTWARE: Patentin Version 3.0
SENGTH: 508
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Best Local Similarity 100.
Matches 130; Conservative
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US-10-146-473-67
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US-10-276-774-2192
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Gaps

24;

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APPLICANT: Zhong, Mei
TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
TITLE OF INVENTION: THE SAME
FILE REPERENCE: 24102-502D
                                                                                                                                                                                                                  184 LGQDDIQLRET----SKPQACPSWPYRFLRKYGSDKGVFSFEAGRKCDSGEGLFAFSSP 238
                                                                                                                                                                                                                                                                           83 RAEELFNMIQEIMQNNSINVVE------EPVVERNNHQTELEVPRTPR 124
                                                                                                                                                                                                                                                                                                                         239 RAPDICGVVAAAIARQRERLPELAMSPPCPLPRALSLPSLEPPGELREVAPGFELPTPRK 298
                                                                                                                                                                          23 LGSGIMELIDTELILYTRKRDSVKWHYLCLRRYGYDSNLFSFESGRRCQTGQGIFAFKCA
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NUMBER OF SEQ ID NOS: 53
SUFTWARE: CuraSeqList version 0.1
SEQ ID NO 6
LENGTH: 331
                                                                        Length 359;
                                                                                                                         47; Indels
                                                                      20.3%; Score 141; DB 9;
28.3%; Pred. No. 8.4e-08;
iive 20; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/307,928A CURRENT FILING DATE: 2002-12-02
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PRIOR FILING DATE: 2001-12-17
PRIOR PELICATION NUMBER: 60/341,540
PRIOR PELLING DATE: 2001-12-17
PRIOR PELLING DATE: 2001-12-17
PRIOR PELLING DATE: 2001-12-20
PRIOR PELLING DATE: 2001-12-30
PRIOR PILING DATE: 2001-12-31
PRIOR PILING DATE: 2001-12-31
PRIOR PILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 60/373,288
PRIOR PILING DATE: 2002-04-17
PRIOR PILING DATE: 2002-05-15
PRIOR PILING DATE: 2002-05-15
PRIOR PILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/381,495
PRIOR PILING DATE: 2002-05-17
PRIOR PILING DATE: 2002-05-17
PRIOR PILING DATE: 2002-05-17
PRIOR PILING DATE: 2002-05-17
PRIOR FILING DATE: 2002-05-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/10307928A Publication No. US20030229016A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boldog, Ferenc L.
Burgess, Catherine E.
Catterton, Elina
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Ji, Weizhen
Kekuda, Ramesh
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Patturajan, Meera
Rieger, Daniel K.
"henoy, Suresh G.
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Gorman, Linda
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Vernet, Corine A.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Alsobrook, John P.
                                                                        Query Match
Best Local Similarity 28.33
Matches 36; Conservative
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Voss, Edward Z
; ORGANISM: Mus musculus
US-09-789-919-58
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APPLICANT:
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APPLICANT: Salcada, Susana
APPLICANT: Salcada, Susana
APPLICANT: Salcada, Herve
APPLICANT: Recipon, Herve
APPLICANT: Scalcada, Herve
APPLICANT: Scalcada, Herve
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
TILE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
FILE REFERENCE: DEX-0283
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/252,189
PRIOR APPLICATION NUMBER: 60/252,189
PRIOR PILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 217
SEQ TWARE: PatentIn version 3.1
SEQ TWARE: PatentIn version 3.1
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APPLICANT: Moore, Kateri
TITLE OF INVENTION: GEBLS THAT REGULATE HEMATOPIETIC BLOOD FORMING STEM
TITLE OF INVENTION: GEBLS AND USES THEREOF
FILE REFERENCE: 2275-1-005
CURRENT PELLING DATE: 201-02-21
NUMBER OF SEQ ID NOS: 96
SEQ ID NOS: 96
SEQ ID NO 58
LENGTH: 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 GSGIMBLIDIELILYTRKRDS-----VKWHYLCLRRYGYDSNLFSFESGRRCQTGQGIF
                                                                                                                                                         1 DIVPDNHRNKFKVINVDDDGNELGSGIMELIDIELILYTRKRDSVKWHYLCLRRYGYDSN
                                                                                                                                                                                                       1 DIVPDNHRNKFKVINVDDDGNELGSGVMELTDTELILYTRKRDSVKWHYLCLRRYGYDSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 AFKCARAEELFNMLOEIMONNSINVVE---EPVVERNNHOTELEVPRTPRTP 126
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                                                        Length 129;
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20.6%; Score 143.5; DB 13; Length
Best Local Similarity 29.5%; Pred. No. 7.4e-08;
Matches 33; Conservative 20; Mismatches 50; Indels
                                                                                                         0; Indels
                                                   Score 679; DB 12;
Pred. No. 5.1e-72;
3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 179, Application US/10001870; Publication No. US20020150924A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 58, Application US/09789919
Patent No. US20020064855A1
GENERAL INFORMATION:
                                                      Ouery Match
Best Local Similarity 97.7%;
Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     121 KTPKTPTTP 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-10-001-870-179
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          JS-09-731-660A-3
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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                                                                 RESULT 10
US-10-106-698-6260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 LGSGIMELTDTE--LILYTRKRDSVKWHYLCLRRYGYDSNLFSFESGRRCOTGOGIFAFK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 CARAEELFUMLOEIMONNSINVVEEPVVERNNHQTEL-----EVPRTPRTFT--TPG 130
                                                                                    Query Match
19.8%; Score 137.5; DB 15; Length 331;
Best Local Similarity 31.5%; Pred. No. 1.9e-07;
Matches 34; Conservative 19; Mismatches 42; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Zing A.

APPLICANT: Wang, Zinwei
TITLE OF INVEWTION: No. US20040048249Alel Nucleic Acids and
TITLE OF INVEWTION: Secreted Polypeptides
FILE REFERENCE: 805A
CURRENT APPLICATION NUMBER: US/10/112,944
CURRENT FILING DATE: 2002-03-28
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR APPLICATION NUMBER: US 09/519,705
PRIOR APPLICATION NUMBER: US 09/519,705
PRIOR PLING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
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                                                                                                                                                                                                                                                                                                                             81 CARAEELFUMLQEIMQNNSINVVEE-----PVVERNNHQTELEVPRT 122
                                                                                                                                                                                                                                                                                                                                                                      213 TREGE----MIYQKVHSATLAIAEQHERLMLEMEQKARLQTSLTEPMT 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 17.3%; Score 120.5; DB 12; Best Local Similarity 29.7%; Pred. No. 2.9e-05; Matches 35; Conservative 16; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 285, Application US/10112944; Publication No. US20040048249A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tang, Y. Tom
APPLICANT: Yang, Yonghong
APPLICANT: Weng, Gezhi
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Xue, Aidong J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang, Jian-Rui
Wehrman, Tom
Ghosh, Malabika
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang, Dunrui
Zhao, Qing A.
Wang, Zhiwei
; ORGANISM: Homo sapiens
US-10-307-928A-6
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; ORGANISM: Homo sapiens
US-10-112-944-285
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Sequence 6260, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polymucleotides and Polypeptides
FILE REFERENCE: PA005F1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT APPLICATION NUMBER: US/202-03-27
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-11-03
PRIOR FILING DATE: 1999-11-03
PRIOR FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SSEQ ID NOS: 8564
SSEQ ID NO 62560
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Sequence 33396, Application US/10029386
PUDLICATION NO. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hansel, David R.
APPLICANT: Hansel, David R.
APPLICANT: HANSION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT PAPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-112-20
NUMBER OF SEQ ID NOS: 34286
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 33396
LENGTH: 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (225)
LOCATION: (225)
FORTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (228)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: MISC FEATURE LOCATION: (229)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-106-698-6260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 MELIDTELILYTRKRDSVK---WHYLCLRRYGYDSNLFSFESGRRCÖTGOGIFAFKCARA 84
   ---CRAVAGAIARQRERLPELTRPQPCPLPRATSLPSLDTPG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Gaps
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16.0%; Score 111.5; DB 14; Length 289;
Best Local Similarity 31.2%; Pred. No. 0.00019;
Matches 20; Conservative 15; Mismatches 26; Indels 3;
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OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
   237 TPCAPDL-----
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PRIOR FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: US 60/138,494
PRIOR FILING DATE: 1999-06-10
PRIOR FILING DATE: 1999-06-10
PRIOR FILING DATE: 1998-08-18
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Version 3.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-10-192-381-5
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OTHER INFORMATION:
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US-09-731-660A-2
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US-10-694-874-3
                                                                                                                                                                                                                LENGTH: 105
                                                                                                                                                                                                                                           TYPE: PRT
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                                                                                                                                                                                         61 LFSFESGRRCQTGQGIFAFKCARAEELFNMLQEIMQNNSINVVE---EPVVERNNHQTEL 117
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APPLICANT: XIAO, Bo
APPLICANT: XIAO, Bo
APPLICANT: LAHAY, Daniel
APPLICANT: LANAHAN, Anthony
TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS TITLE OF INVENTION: AMENDED)
TITLE OF INVENTION: AMENDED
TITLE OF INVENTION: AMENDED
TITLE OF INVENTION NUMBER: US/10/192,381
CURRENT APPLICATION NUMBER: US/09/377,285
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; Sequence 2340, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INPORMATION:
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; CURRENT EMERGENEE: 105/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SEQ ID NOS: 4360
; SEQ ID NOS: 3400
; FEMALIE DATE: 2000-06-07
; PRIOR PRIVERE: PATENTIN VET. 3.1
                                                                                Score 95.5; DB 14; Length 268; Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 268;
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Publication No. US20030170807A1
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: WORLEY, Paul
        ; OTHER INFORMATION: SWISSPROT HIT: P56945, EVALUE 2.00e-03
US-10-029-386-333396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.7%; Score 95.5; DB 15; 27.5%; Pred. No. 0.013; tive 16; Mismatches 31;
                                                                                Query Match
Best Local Similarity 27.5%; Pred. No. 0.01.
Matches 19; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/138,426
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PRIOR APPLICATION NUMBER: US 60/138,493
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Best Local Similarity 27.5%
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                  62 AEGKLPSPP 70
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CRGANISM: Homo sapiens
US-10-264-049-2340
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APPLICANT: KOUHARA, HARUHIKO
APPLICANT: SPIYAK-KROIZMAN, TALY
APPLICANT: SPIYAK-KROIZMAN, TALY
APPLICANT: SPIYAK-KROIZMAN, TALY
APPLICANT: SCHLESSINGER, JOSEPH
TITLE OF INVENTION: ADAPTOR PROTEIN PRS2 AND RELATED PRODUCTS AND METHODS
FILE REFERENCE: 038602/1023
CURRENT APPLICATION NUMBER: 08/99/731,660A
CURRENT FILING DATE: 2000-12-08
PRIOR PILING DATE: 1997-12-01
PRIOR APPLICATION NUMBER: 60/932,093
PRIOR FILING DATE: 1996-12-03
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 LRRYGYDSNLFSFESGRRCQTGQGIFAFKCARAEELFNMLQEIMQNNSINVVEEPVVERN 111
                                                                                                        52 LRRYGYDSNLFSFESGRRCQTGQGIFAFKCARAEELFNMLQEIMQNNSINVVEEPVVERN 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
11.2%; Score 78; DB 12; Length 114;
Best Local Similarity 30.0%; Pred. No. 0.49;
Matches 21; Conservative 7; Mismatches 20; Indels 3
Score 78; DB 14; Length 105;
Pred. No. 0.44;
7; Mismatches 20; Indels
                                                                                                                                              59 IRRCGHSENFFFIEVGRSAVTGPGEFWMQ---
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09731660A Publication No. US20020086972A1 GENERAL INFORMATION:
        11.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Unknown Organism
     Query Match
Best Local Similarity 30.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 MHETILEAMR 106
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APPLICANT: POLAKIEWICZ, Roberto
APPLICANT: LI, Yu
APPLICANT: WU, Jiong
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR PHOSPHORYLATED IRS-1/2 (Ser1101/Ser1149)
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CURRENT RELIGION NUMBER: US/10/694,874
CURRENT FILING DATE: 2003-10-28
PRIOR FILING DATE: 2002-10-30
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 3
LENGTH: 1231
FYPE: PRI
TYPE: PRI
CREATION: CREATION NUMBER: CREATION NOS: 11
SEQ ID NO 3
LENGTH: 1231
TYPE: PRI
CREATION: CREATION NUMBER: CREATION NOS: 11
SEQ ID NO 3
LENGTH: 1231
TYPE: PRI
CREATION: CREATION NUMBER: CREATION NOS: 11
SEQ ID NO 3
LENGTH: 1231
TYPE: PRI
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11.2%; Score 78; DB 16; Length 1231;
Best Local Similarity 30.0%; Pred. No. 13;
Matches 21; Conservative 7; Mismatches 20; Indels 22
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6 B 6

Search completed: August 2, 2004, 09:40:46 Job time : 69.2763 secs

112 NHQTELEVPR 121 |:| | | | 244 MHETILEAMR 253

Run on:

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RESULT
                                                                                                                                                                                                                                                                                                                                                                  Command line parameters:
-MODEL=frame+ p2n.model - DEV=xlh
-Q-(cgn2_1/USPTO_spool/US09757415)runat_02082004_101230_6685/app_query.fasta_1.526
-Q-(cgn2_1/USPTO_spool/US09757415)runat_02082004_101230_6685/app_query.fasta_1.526
-Q-(cgn2_1/USPTO_spool/US09757415/runat_02082004_101230_6685/app_query.fasta_1.526
-UNINS=bits -STRAT=1 - END=-1 - MATRIX=blosum62 - TRANS=bluman40.cdi - LIST=45
-UNINS=bits - STRAT=1 - END=-1 - MATRIX=blosum62 - TRANS=bluman40.cdi - LIST=45
-UNINS=bits - STRAT=1 - MDE=10 - MATRIX=BRAZ=100 - TRR_MIN=0 - ALIGN=15 - MODE=LOCAL
-USER=US09757415_@CGN 1 1 3851_@runat_02082004_101230_6685 - NCPU=6 - ICPU=3
-NO MAAP - LARGEQGERS - NEG SCORES=0 - WAIT - DEPELOCK=100 - LONGLOG
-DEV TIMEOUT=120 - WARN TIMEOUT=30 - THEABAS=1 - KORPOP=10 - KGAPEXT=0.5 - FGAPOP=6
                                                                                                    (without alignments)
1182.153 Million cell updates/sec
                                                                                                                                         US-09-757-415A-1_COPY_11_140
696
1 DTVPDNHRNKFKVINVDDDG......NNHQTELEVPRTPRTPTFG 130
                                                                                   August 8, 2004, 19:45:10 ; Search time 4766.38 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                         using frame_plus_p2n model
                                                                                                                                                                                                                                                                                           3470272 seqs, 21671516995 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                    BLOSUM62
Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
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BC055344 Mus muscu
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BC01611 Homo sapi
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AC10129 Rattus no
AC112658 Rattus no
AC112668 Rattus no
AC11269 Homo sapi
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ALIGNMENTS

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AATGAGTTAGGTTCTGGCATAATGGAACTTACAGACACACAGAACTGATTTATACACCCGC 155
                                                     LysargaspSerValLysTrpHisTyrLeuCysLeuArgargTyrGlyTyrAspSerAsn 60
                                                                         156 AAACGTGACTCACTAAAATGGCACTTCTGCCTGCGACGCTATGGCTATGACTCGAAT
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                      96
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KEYWORDS
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       AF036717 1532 bp mRNA linear PRI 30-JUL-1999
Homo sapiens FGFR signalling adaptor SNT-1 mRNA, complete cds.
AF036717
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LILYTRKRDSDYKWHYLCLEKRYGYDSNELEFESGSRCGYGGGGTFFRKCARABEELFNMLQ
ENGNNSINVVERPVVERNHYGTELFYPRTPTTPGFAAGNLPNGYPRYFSGDAS
SHPSSRHPSVGSARLPSVGESTHPLLVAEGVHTYVNTTGVQEERKNRTSVHVPLEA
SKYNBRSSTFKEEPSSIEDREPOILEBPGVRFALGPFPVGYGDMFKXGTAGLGGDQV
SGSGANNTEWDTGYDSDERRDAPSVNKLLYNENINGLSPFSAGGVRACHITSTSDTG
NINNSAQRRTALLNYEMLPSLEPPVWEARKLSRDBDDNLGPKTPSLNGYHNNLDPMHNY
                                                                                                                                               1 (bases 1 to 1532)
Xu,H., Lee,K.W. and Goldfarb,M.
Novel recognition motif on fibroblast growth factor receptor mediates direct association and activation of SNT adapter proteins J. Biol. Chem. 273 (29), 17987-17990 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VNTENVTVPASAHKI EYSRRRDCTPTVFNFDI RRPSLEHRQLNYI QVDLEGGSDSDNP
QTPKTPTTPLPQTPTRRTELYAVI DI ERTAAMSNLQKALPRDDGTSRKTRHNSTDLPM
                                                                                                                                      Eukaryota, Metazoa; Chordata, Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AspThrValProAspAsnHisArgAsnLysPheLysValIleAsnValAspAspAspGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACACTGTCCCAGATAACCATCGGAACAAGTTTAAGGTCATTAATGTGGATGATGATGGT
                                                                                                                                                                                                                                                                                                                                                Submitted (04-DEC-1997) Brookdale Center for Developmental Molecular Biology, Mr. Sinal School of Medicine, 1 Gustave Place, New York, NY 10029, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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/db_xref="G1:2708628"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1532
130
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/note="encodes myristoylation motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-757-415A-1_COPY_11_140 (1-130) x AF036717 (1-1532)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="similar to murine FRS2"
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/chromosome="12"
/map="12p15"
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1. 1532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51. .398
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/note="encodes PTB domain"
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Xu,H., Lee,K. and Goldfarb,M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="SNT-1"
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gene="SNT-1"
                                                                     AF036717.1 GI:2708627
                                                                                                        Homo sapiens (human)
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100.00%
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Best Local Similarity:
Query Match:
DB:
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AF036717
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                       ORGANISM
                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
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PUBMED
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JOURNAL
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21 AsnGluLeuGlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArg 40

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 1840)

S traushers, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Altschul, S.F., Zeeberg, B.L., Bhat, N.K., Altschul, S.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleron, M., Soarses, M. B., Bonaldo, M.F., Casarant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Morkernan, K.J., Mallah, J.A., Quanatane, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Vilalon, D.K., Waizny, D.M., Sodersren, E.J., Luly, X., Gibbs, R.A., Fahey, J., Helton, B., Sacreia, A.M., Madan, A., Rodriques, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Krzywinski, M.I., Stalska, U., Smailus, D.E., Butterfield, Y.S., Krzywinski, M.I., Stalska, U., Smailus, D.E., Generation and initial analysis of more than 15,000 full-length human and mouse conka sequences

M.D. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC021562
Homo sapiens fibroblast growth factor receptor substrate 2, mRNA
CONA clone MGC:31881 IMAGE:4556225), complete cds.
                                                                                                                                                                                                                                                                                                                                                                             216 CICITITCITITGAAAGIGGICGAAGGIGICAAACIGGACAAGGAAICTITGCCTITAAG 275
                                                                                                                                                                  CysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGluIleMetGlnAsnAsnSerIle 100
                                                                                                                                                                                                                                                 276 TGTGCCCGTGCAGAAGAATTATTTAACATGTTGCAAGAGATTATGCAAAAATAATAGTATA 335
                                                                                                                                                                                                                                                                                                                                     101 AsnValValGluGluProValValGluArgAsnAsnHisGlnThrGluLeuGluValPro 120
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Submitted (14-ZAN-2002) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
LeuPheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGly1lePheAlaPheLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ArgThrProArgThrProThrThrProGly 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BC021562
BC021562.1 GI:18204300
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mans misculus

In (bases 1 to 5701)

Altschuly, Strucheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Altschuly, S.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschuly, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Mans, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Schaeferon, M., Soares, M.M. B., Bonaldon, F., Casavant, T.L.,

Scheerz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Morley, K.C., Mallahy, S.J., Boarsk, S.A., McEwant, P.J.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Fahey, J., Hellton, E., Ketteman, M., Madan, A., Schmerch, S.,

Boutfard, G.G., Blakesieley, R.W., Towoman, J.W., Green, E.D.,

Boutfard, G.G., Blakesieley, R.W., Towoman, J.W., Schmerc, J., Myers, R.M.,

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

RD. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BC043109 5701 bp mRNA linear ROD 11-DEC-2003 Mus musculus fibroblast growth factor receptor substrate 2, mRNA (CDNA clone MGC:58030 IMAGE:6406912), complete cds. BC043109
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benaldo,Mr., Akabogu,I., Balir,T., Crouch,Kr., Davis,A.,
Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
                                                                                                                                                                                                                                                                                           101 ASDValValGluGluProValValGluArgASDASDHisGlnThrGluLeuGluValPro 120
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                                                                                                                                                                                                             577 ARTGIGGIGGAAGAGCCAGIIGIAGAAAGAAATAAICAICAGACAGAAIIGGAAGICCCI 636
397 AAACGTGACTCAGTAAATGGCACTACCTCTGCCTGCGACGCTATGGCTATGACTCGAAT 456
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Submitted (09-JAN-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: MGC help desk
Email: cgapbs.rdmail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and I
Thomas L. Casavant.
Web site: http://genome.ulowa.edu
                                                    LeupheSerpheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePheAlaPheLys
                                                                                                      457 CICTITICITITIGAAAGIGGICGAAGGIGTCAAACIGGACAAGGAAICTITIGCCTITAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                  121 ArgThrProArgThrProThrThrProGly 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       637 AGAACACCTCGAACACCTACAACTCCAGGA 666
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DEFINITION
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JOURNAL
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VERSION
KEYWORDS
SOURCE
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BC043109
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SHPSSRHPSVGSRARLPSVGEBSTHPLLVAEEQVHTYVNTTGVQBERKRRTSVHVPLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVSNAESSTPKEEPSSIEDRDPQILLEPEGVKFVLGPTPVQKQLMEKEKLEQLGRDQV
SGSGANNTWDTGYDSDERRDAPSVNKLVYENINGLSIPASGVRRGRLTSTGTSDTQ
NNNSAQRRTALLNYENLESLPPWEARKLSRDEDDNLGPKTPSLUGYHNNLDPWHVY
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                                                                                                                                                                                                                                                                                                                             found
   BC Cancer Agency, Vancouver, BC, Canada
Lifeobogosco, Com
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Letticia Hislao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Danas Gamilus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 40 Row: e Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21314643. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277 GACACTGTGCGAGATAACCATGGGAACAAGTTTAAGGTCATTAATGTGGATGATGATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        337 AATGAGTTAGGTTCTGGCATAATGGAACTTACAGACACAGAACTGATTTTATACACCCGC 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AsnGluLeuGlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AspThrValProAspAsnHisArgAsnLysPheLysValIleAsnValAspAspAspGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRS2alpha, SNT1, FRS2A, SNT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="IRS; Region: PTB domain (IRS-1 type)"
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="synonyms: SNT-1, F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAH21562.1"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 5792)

Altschul, S. L., Feingold, E. A., Grouse, L. H., Derge, J. G., Klausner, R. D., Collins, F. S., Wagner, L., Schemer, C. M., Schuler, G. D., Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhar, N. K., Hopkins, R. F., Jordan, H., Moore, T. Max, S. I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K. J. Farmer, A. A., Rubin, G. M., Hong, L., Stapleron, M., Soares, W. B., Bonaldo, M. F., Casavant, T. L., Stapleron, M., Soares, W. B., Bonaldo, M. F., Casavant, T. L., Stapleron, M., Sarmschin, M. J., Usdin, T. B., Toshiyuki, S., Carninci, P., Prange, C., Rah, S. S., McGin, T. B., Toshiyuki, S., Garninci, P., Mullahy, S. J., Bosak, S. A., McEwan, P. J., Malek, J. A., Gunarane, P. H., Richards, S., Morley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W., Villalon, D. K., Mullahy, S. J., Bosak, S. J., Lu, X., Gibbs, R. A., Sahey, J. Halton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchaz, A., Whiting, M., Madan, A., Young, A., Schotin, S. Maring, M., Madan, A., Young, A., Shevchenko, Y. Butterfield, Y. S., Krzywinski, M. I., Skalska, U., Santus, D. E., Schnerch, A., Schein, J. B., Jones, S. J., and Marra, M. A., Goren, E. D., Generation and initial analysis of more than 15,000 full-length
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Contect: MGC help desk
Email: cgapbs-r@mail.nih.gov
Itsue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
Thomas L. Casavant.
Web site: http://genome.uiowa.edu
Contect: bento-soares@ulowa.edu; tom-casavant@ulowa.edu
Contect: bento-soares@ulowa.edu; tom-casavant@ulowa.edu
Bonaldo,M.F., Akabogu,I.M. Bair,T., Bair,J., Grouch,K., Davis,A., Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K., Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                BC055334 Sibroblast growth factor receptor substrate 2, mRNA (CDNA clone MGC:64739 IMAGE:6830555), complete cds.
                                                                                           626 IGTGCCCGTGCAGAAGAATTATTTAACATGTTGCAAGAGATTATGCAAAATAATAGTATA 685
                                                          101 AsnValValGluGluProValValGluArgAsnAsnHisGlnThrGluLeuGluValPro 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (22-UUL-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: Plate: Row: Column: Of This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
                                                                                                                                                                                                                          746 AGGACACCTCGGACACCTACAACTCCAGGG 775
                                                                                                                                                                                121 ArgThrProArgThrProThrThrProGly 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BC055334.1 GI:33244012
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AUTHORS
TITLE
JOURNAL
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AUTHORS
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BC055334
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KEYWORDS
SOURCE
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COMMENT
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                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: Plate: Row: Column: 0
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LILYTRKRDSVKWHYLCLRRYGYDSNILFSFESGRRCQTGQG1FAFKCARAEELFNMLQ
EIMONNSINVVEEPVVERSSHQTELEVPRTPRTPTTFGLGAQNILPNGYPRYPSFGDAS
SHPSSRHPSVGSARLPSVGERSTHPLLVAEEQWHTYNYTGYDGERKNRASVHVPPEA
RVSNAESNITPKEEPSNPEDRD DQVLLKPEGVRFVLGPTPVQKQLMEKEKLEGLGKXDPV
SGSGAGNTEWDTGYDDERRRYPPVNKLYYENINGLSIPSASGVRKGRILTSTSSDTO
NINNSAQRRPALLNYENLPSLLPPVWEARKLSYBDDDNLGPKTPSLLNGYHNNLDPMHNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="LocusID:327826"
/translation="MGSCCSCPDKDTVPDNHRNKFKVINVDDDGNELGSGVMELTDTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VNTENVTVPASAHKI DYSKRRDCTPTVFNFDI RRPSLEHRQLNYI QVDLEGGSDSDNP
QTPKTPTTPLPQTPTRRTELYAVI DI ERTAAMSNLQKALPRDDGTSRKTRHNSTDLPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      386 GACACTGTCCCAGATAACCATCGGAACAAGTTTAAGGTCATTAATGTGGATGATGATGGTGG 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 CysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGluIleMetGlnAsnAsnSerIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 506 AAACGGGACTCGGTAAAATGGCACTACCTCTGCCTACGACGATACGGCTATGACTCAAAT 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              566 CTGTTTTCTTTTGAAAGTGGTCGAAGGTGTCAGACTAGACAAGGAATTTTTGCTTTTAAG 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 AsnGluLeuGlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArg 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 LysargaspSerVallysTrpHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsn 60
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                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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/clone="MGC:58030 INAGE:6406912"
/tissue type="Brain, enriched mouse brain 12.5dp"
/clone lib="WHH BMAP_FOO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="IRS; Region: PTB domain (IRS-1 type)"
/db_xref="CDD:pfam02174"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="synonyms: 4732458E18, SNT1"
/db_xref="LocusID:327826"
356. .1882
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product="Frs2 protein"
protein_id="AAH43109.1"
db_xref="GI:27695420"
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   Casavant, T., Soares, M.B.
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233. .1762
/gene="xFRS2"
/note="involved in early embryogenesis in cooperation with
the Src family kinase Laloo"
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db xref = T01:14588670"

/db xref = T01:14588670"

/LINTRKRDSVWAPYLCIRRYGYDSNLFSFESGRRCQTGQGJFAFKCARAEELFNMLQ

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RAPSCRHPSVGSTRLSSVGESGTHPLLVPEDHYTPGFSGGSGVPNGYPRYSFGGRASS

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ONVNNSAQRRTALITYTGYDSDERREISSSNKMYTPANTALISSSGGLRRGNVPPTSTDI

ONVNNSAQRRTALITYDGYDSDERREISSSNKMYTPANTALISSSGGLRRGNVPPTSTDI

VNNTNNSAQRRTALITYDGYDSDERREISSSNKMYTPRDFRIPPRHY

VNNTNNSAQRRTALITYDGYDSDERREISSDSDI
                                                                                                                                                                                                                                                                                                   Kusakabe,M., Masuyama,N., Hanafusa,H. and Nishida,E.
Xenopus FRS2 is involved in early embryogenesis in cooperation with
the Src family kinase Laloo
EMBO Rep. 2 (8), 727-735 (2001)
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4"
                                                                             VRT 22-FEB-2002
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Kusakabe, M., Masuyama, N. and Nishida, E.
Subrect Submission
Submitted (30-UNN-2001) Eisuke Nishida, Graduate school of
Biostudies, Kyoto University, Department of Cell and Developmental
Biology, Kitashirakawa, Sakyo, Kyoto 606-8502, Japan
(E-mail:15017)40sakura.kudpc.kyoto-u.ac.jp, Tel:81-75-753-4230,
Fax:81-75-753-4235)
Location/Qualifiers
                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 GAAACTATCCCAGATAACCAACAAACAGATTTAAGGTTATTAACGTTGATGATGATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ASDThrValProAspAsnHisArgAsnLysPhelysVallleAsnValAspAspAspGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 AsnGluLeuGlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArg
                                                                  AB064525 2280 bp mRNA linear
Xenopus laevis xFRS2 mRNA for FRS2, complete cds.
AB064525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2280
117
7
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Mismatches:
Indels:
811
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Matches:
                                                                                                                                                                            Xenopus laevis (African clawed frog)
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Xenopus laevis"
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782 AGGACACCTCGGACACCTACAACTCCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product="FRS2"
                                                                                                                                     AB064525.1 GI:14588669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="xFRS2"
                                                                                                                                                                                                                                                                Xenopodinae; Xenopus.
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616.50
95.38%
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Best Local Similarity:
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DB:
                                                                                            DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
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                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE
PUBMED
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                                                                                                                                                                                                                                                                                    REFERENCE
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                                                            AB064525
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                                        RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LILYTRKRDSVKWHYLCLRRYGYDSNLFSFESGRRCOTGGGIFAFKCARAEELFNMLQ
BIDQINSINTWUERPWERSSHQTELFUPPTROFTAGGLGAQNLENGYRPRYSFGDAS
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RVSNAESNTPKEEPSNFEDRDPQVLLKPEGVRFYLGPTPVQKQLMEKEKLEQLGKDPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGSGAGNTEWDIGYDSDERRDVPPVNKLVYENINGLSIPSÄSGVRRGRLISTSTSDTQ
NINBAQNERPALLNYENLEPEPPVMBARKLSKBIDDDIGKRYFBLIGYRINNLDPPRHNY
NINTBNYTVPASAHKI DYSKRRDCTPTVFNPINDIRRPSILBHRQIMY IQVDLEGGSDSDNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGluIleMetGlnAsnAsnSerIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AsnValValGluGluProValValGluArgAsnAsnHisGluThrGluLeuGluValPro 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     542 AAACGGGACTCGGTAAAATGGCACTACCTCTGCCTACGACGATACGGCTATGACTCAAAT 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rerececerecagaagarrarraacarerrecaagagarrarecaaaaraaragrara 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AspThrValProAspAsnHisArgAsnLysPheLysVallleAsnValAspAspGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CIGITITICITITIGAAAGIGGICGAAGGIGTCAGACIGGACAAGGAAITITITIGCITITIAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AsnGluLeuGlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       482 AATGAGCTAGGCTCTGGTGTGATGGAACTCACAGACACAGAGCTGATTCTGTACACCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LysArgAspSerValLysTrpHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsn
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/note="IRS; Region: PTB domain (IRS-1 type)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5792
127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       m 0 0 0
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                    /note="Vector: pYX-ASC"
1. .5792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
Location/Qualifiers
                                                            /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.93e-77
685.00
100.00%
97.69%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        422
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DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.:
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FEATURES
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20

382

be found

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Contact: XGC help desk

Contact: XGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procuremen: Dr. Igor Dawid

CDNA Library Parzayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: http://www.nisc.nih.gov/

Contact: nisc_gregenhgri.nih.gov/

Contact: nisc_gregenhgri.nih.gov/

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

Blakesley,R.W., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,

McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,

Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,

Young,A., Zhang,L.-H. and Green,B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ONVANSAORRTALINYENLPSLPPWETRRSSREEDDSLGPKTPSLNGFHSNLDPMHN
YVATENVTVPLSAHKVEFSRRDCSPTVFNPDIRRPSLEGRQLNYIQVDLEGGSDSDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /trānslation="WGSCCSCPDKETIPDNOONRFKVINVDDDGNELGSGIMELRENE
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NNDGSSCPNNTELDTGYDSDERREISSNKMVYENLNGLSISSSGLRRGRVVPPISTDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 97 Row: b Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14588669. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPSSRHPSVGSTRLPSVGEESTHPLLVPEDHVHTYVNTSGVPEDQKSRPNAPPAQEVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Xenopus laevis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="synonym: MGC52516"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3017
|gene="frs2-prov"
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95.38%
90.00%
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20892-7510, USA
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Best Local Similarity:
Query Match:
DB:
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                          REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
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                                                    COMMENT
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Klausherg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausherg, R.L., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schenen, C.M., Schuler, G.B.,
Hopkins, R.F., Jordan, H., Moore, T., Wax, S.I., Wang, J., Hsieh, P.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, W.M. B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
McKernan, K.J., Mallahy, S.J., Bosak, S.A., McEwant, P.J.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vilalon, D.K., Wanny, D.M., Sodergren, E.J., Lux, Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bucterfield, Y.S., Kzzywinski, M.I., Schmern, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Generation and mouse cDNA sequences

N.D. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Xenopus laevis sucl-associated neurotrophic factor target (FGFR signalling adaptor), mRNA (cDNA clone MGC:52516 IMAGE:5570479),
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Direct Submission (14-PB-2003) National Institutes of Health, Xenopus Gene Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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Klein, S.L., Strausberg, R.L., Wagner, L., Pontius, J., Clifton, S.W.
and Richardson, P.
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                                                             LeuPheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePheAlaPheLys
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/note="IRS; Region: PTB domain (IRS-1 type)"
/db_xref="CDD:pfam02174"
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Mismatches:
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PAT 27-AUG-2002
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PQTPKTPTTPLPQTPTRRTBLYAVIDIBRTAAMSNLQKALPRDDGTSRKTRHNSTDLP
M"
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11 (bases 1 to 76.
10 (b. J., Scanlan, M.J., Stockert, E., Gure, A., Chen, Y.T., Gout, I., OGhare, M., Obata, Y., Pfreundschuh, M., Tureci, O. and Sahin, U. Cancer-associated nucleic acids and polypeptides
LUDWIG INSTITUTE FOR CANCER RESEARCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO1N33/574, A61K38/00, A61K39/395, A61K39/395, A61K45/00, A61K48/00,
                                                                                                                                                                                                                                                                                                                                                                           91 AATGAGCTTGGCTCTGGCATAATGGAATTGACCGAAAATGATCTCATCTTATACACTCGC
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                                                                                                                                                                                                                                                                             1 AspThrValProAspAsnHisArgAsnLysPhelysValIleAsnValAspAspGly
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PN JP 201516009-A/6

PD 25-SEP-2001

PF 15-JUL-1997 US 60/061599

10-OCT-1997 US 60/061765, 10-OCT-1997 US 60/061599

11-OCT-1997 US 60/061765, 10-OCT-1997 US 08/948705 PR

11-OCT-1997 GB 9721697.2, 22-JUN-1998 US 09/102322 PI

J OLD, MATTHEW J SCANLAN, ELISABETH: STOCKERT, ALI GURE, YAO PI
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Homo sapiens (human)
Homo sapiens
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AF390895
AF390895.1 GI:18033969
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/protein_id="AAL57304.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSS PEGIHGHGEPPVPERDPQVILEPDGVKFVLGPTPVQRQLIEKKKLETIBQHQDSV
NNGESSCPNNTEWDIGYDSDEHRETPSNKMVCENLNGLSSLSSAVQRGRVVPPISTDI
QNVNNSAQRRTALINYENLPSLPPVWETRKPSREEDDSLGPKTPSLNGFHSNLDPMHN
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EIMONNTISVVEBPVVERNPQTBLDVPRTPRTPTPGFSGSGVPNGYPRYPSVGEASS
HPSSRHPSVGSTRLPSVGESTHPLLVPEDHVHTYVNTSGVQEDQKQRPNVPPAQEVR
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                                                                                AAGAGAGATICIGICAAGIGGCCITACCICIGCIIGCGACGCIAIGGATACGAITCAAAC 383
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                     204 GAAACTATCCCAGATAACCAACAAAACAGATTTAAGGTTATTAACGTTGATGATGATGGT
                                                        AsnGluLeuGlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArg
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MD 21702, USA
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note="FGFR signaling adaptor FRS2"
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Akagi,K., Mood,K. and Daar,I.O.
Direct Submission
Submitted (12-UN-2001) Regulation of
National Cancer Institute, Frederick,
Location/Qualifiers
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Xenopus laevis

    .1612
    organism="Xenopus laevis"

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/db_xref="taxon:8355"
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Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, E.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchamn, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
L. Proc., Natl. Acad. Sci. U.S.A., 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/tissue_type="Brain, glioblastoma with EGFR amplification"
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/lab_host="DHOS"
/note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 12 Row: 1 Column: 14 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 5730058. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="syronyms: SNT2, FRS2B, MGC17167, SNT-2, FRS2beta"

db_xref="LocusID:10817"

/db_xref="MIM:607744"
                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (10-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.K., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: MGC help desk Famil: Graphs - Famil: Graphs - Famil: nih.gamal: Graphs - Famil: nih.gamal: Bayla N. Louis, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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AUTHORS
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JOURNAL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordates; Crarrhini; Hominidae; Homo.

I (bases 1 to 2031)
Strausberg, E.D., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, K.D., Collins, F.S., Wagner, L., Shemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRI 07-0CT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COTX.4/82,COTX.6/32,C12N15/09//COTX.16/46,C12P21/08,A61X37/02,C12N15/00
Cancer-associated nucleic acids and polypeptides. FH Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 rIleAsnVal-ValGluGlu-ProVal-ValGluArgAsnAsnHisGln--ThrGluLeu 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    359 GACACTGTCCCAGATAACCATCGGAACAAGTTTAAGGTCATTAATGTGGATGATGATGATGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 AsnGluLeuGlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 sCysAlaArgAla-GluGluLeuPheAsnMetLeuGln-GluIleMetGln-AsnAsnSe
                                                                                                                                                  /organism='Homo sapiens (human)'
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 GluValPro---ArgThrProArgThrProThrThrPro 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAGTCCCTAANAACAACCTCGAAACAACTACAACTCCA 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-757-415A-1_COPY_11_140 (1-130) x BD079340 (1-766)
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Matches:
Conservative:
Mismatches:
Indels:

    .766
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517.50
87.77$
86.33$
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     A61P35/00,
PC C07K14,
PC C12N15,
CC Cancer-
                                                                                                                                     source
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Best Local Similarity:
Query Match:
DB:
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AUTHORS
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BC010611
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/protein id="AAB92555.1"

/db xerf="FGT:2708630"

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PRRLSTSSLRHPSLGBESTHALIAPDEQSHTYVNTPASEDDHRRGRHCLQPLPEGQAP
                                                                                                                                                                                                                                                                        BC014819 2150 bp mRNA linear ROD 06-OCT-2003 Mus musculus fibroblast growth factor receptor substrate 3, mRNA (cDNA clone MGC:25496 IMAGE:4506982), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 GTGGAGCTGGGCTCTGGGGTGATGGAGCTGACGCAGAGTGAGCTGGTGCTGCACTTGCAT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 CysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGluIleMetGlnAsnAsnSerIle 100
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Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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71
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Matches:
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|note="encodes PTB domain"
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BC014819.1 GI:15928711
MGC.
                     137. .1615
/gene="SNT-2"
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/gene="SNT-2"
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86.26%
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Homo sapiens FGFR signalling adaptor SNT-2 mRNA, complete cds.
AF036718
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I (Bases 1 to 2077)

Xu, H., Lee, K.W. and Goldfarb, M.
Novel recognition motif on fibroblast growth factor receptor mediates direct association and activation of SNT adapter proteins J. Biol. Chem. 273 (29), 17987-17990 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               AsnGluLeuGlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArg 40
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Xu,H., Lee,K. and Goldfarb,M.
Direct Submission
Submitted (04-DEC-1997) Brookdale Center for Developmental and
Molecular Biology, Mt. Sinal School of Medicine, 1 Gustave Levy
Place, New York, NY 10029, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysArgAspSerValLysTrpHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsn
                                                                                                                                                                                                                                                                                                                                                              AspThrValProAspAsnHisArgAsnLysPheLysValIleAsnValAspAspAspGly
/note="IRS; Region: PTB domain (IRS-1 type)"
/db_xref="CDD:pfam02174"
                                                                                                                                                                                                                                                                                                           US-09-757-415A-1_COPY_11_140 (1-130) x BC010611 (1-2031)
                                                                                                                                                    Matches:
Conservative:
Mismatches:
Indels:
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/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/tissue type="placenta"
1. .2077
                                                                                                                              ength:
                                                                                                                                                                                                                                                          Gaps:
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70.23%
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LVLHIHORBAVRMPYLCLRRYGYDSNLFSFESGRRCOTGOGIFAFKCSRAEDIFNLLD
DLMQCNSINVTEEPVIITRSSHPPELDLPRGPPQPAGYTVSGFSNGFPGCPGEGPRFS
SAPRRPSTSSLRHPSPGEESTHTLIASEBQSHTYVNTPTGDEDGRSRHCLQPLPEGRV
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      translation="MGSCWSCLDRDSVPHNHPTKFKVTNVDDEGVELGSGVMELTQSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323 GTGGAGTTGGGCTCGGGGGTGATGAGCTGACCCAGAGTGAGCTGGTGATGACCTGCAC 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383 CAGCGGGAAGCTGTCCGCTAGCCTACCTCTGCCTGCGGCGCTATGGCTACGACTCCAAT 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           503 IGTICGAGGGCAGAGGACATCTICAACCTGCTGGAGGACCTCATGCAGGAACGTAACAGCATC 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 GACAGCGTGCCGCACAACCACCTACCAAGTTCAAGGTGACCAATGTGGATGATGAAGGG 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 CysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGluIleMetGlnAsnAsnSerIle 100
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Human chromosome 12p15 BAC clone CIT987SK-99D8 complete sequence.
U91327.1 GI:1871209
HTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 AsnGluLeuGlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArg 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LeuPheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePheAlaPheLys 80
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 129252)
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/note="IRS; Region: PTB domain (IRS-1 type)"
/db_xref="CDD:pfam02174"
                                                                                                                                                                                                                                         SSDSYAVIDLKKTAAMSDLQRALPRDDGAVRKTRHNSTDLPL"
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Pred. No.:
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                                           1 (bases 1 to 2150)

Strausberg, L., Felogold, E.A., Grouse, L.H., Derge, J.G.,
Klausherg, R.L., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Batt, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Mans, S.L., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Rah, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunarane, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madni, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 31 Row: m Column: 15 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21450352. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Nobiste: http://www.hgsc.bcm.tmc.edu/cdna/
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2150)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="fibroblast growth factor receptor substrate 3" /protein id="AAH14819.1" /protein id="AAH14819.1" /db_xref="locusID:107971" /db_xref="locusID:107971"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (01-CCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-romail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/db_xref="taxon:10090"
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/tissue_type="Eye, retina, mouse strain C57Bl\6"
/clone=Ibb=NIH MGC 94"
/lab host="DH108"
/note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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/db_xref="LocusID:107971"
/db_xref="MGI:2135965"
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/organism="Mus musculus"
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Strausberg, R.
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PRI 10-JAN-2000

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Submitted (21-AdG-1997) The Institute for Genomic Research, 9712

Medical Center Dr., Rockville, MD 20850, USA

BAC clone CIT987SK-9998 is located in band 12p15 of chromosome 12.

Genes were identified by a combination of five methods: XGRAIL

Gavailable by anonymous ftp from arthur.epm.ornl.gov), Genefinder

(available by anonymous ftp from colin@u.washington.edu), GENSCAN

(available by anonymous ftp from colin@u.washington.edu),

searches of the EST database at TIGR

(http://www.tigr.org/fdb/ndc/hcd.html) and searches against a

(http://www.tigr.org/fdb/ndc/hcd.html) and searches against a

peptide database. Repeats were identified using RepeatMasker (Smit,

A.F.A. and Green, P. unpublished,

http://ftp.genome.washington.edu/rm/RepeatMasker.html.
                                                                                                                                                   Submitted (04-MAR-1997) The Institute for Genomic Research, 9712 Medical Center Nockville, MD 20850, USA 4 (bases 1 to 12922) Adams, M.D., Loftus, B.J., Zhou, L., La Bombard, M., Kim, U.J. and Venter, J.C.
                                                                                                          Adams, M.D., Loftus, B.J., Phillips, C.A., Zhou, L., Brandon, R. and
   2 (bases 1 to 129252)
Adams, M.D. Loffus, B.J., Zhou, L., Phillips, C., Brandon, R., Fuhrmann, J., Kim, U.J., Kerlavage, A.R. and Venter, J.C. Chromosome 16p12 BAC Clone CIT9875K-99D8 complete sequence
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76	OY 76	108275 ACACCTAGGGACTTTCCAAGGGCCTGTTACATGGCAAATGATCACCTTGGAATAGTGAG 76	108335 TIGGGCICCCCCGCTGTTAGAAAAAGACTAGCGTAAGTGCGCAGGICTTGATTTCATT 76 108395 AGCTTTATTTTGGGCCATCTCCCTTAGATGAAATGAAAT	108515 TCTGACTCGGTGCGTAGAATGCTTACAATTCTGCTGTTTGTCAAGTGTTCCTATA 1085 77	108635 GCCIIIANGIGICCCCICCAANAGATIAIIIAACAAGAGATATIACAAGAGATATIACAAGAGATATIACAAGAGATATIACAAGAGATATIACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	ACO18921/C ACO18921 ACO18921 ACO18921 BACO18921 BACO18921 BACO18921 BEFINITION Homo sapiens 12 BAC RPI1-956E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence. ACCESSION ACO18921.22 GI:16327992 KEYWORDS HTG. SOURCE Homo sapiens (human) ORGANISM HTG. Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; REFERENCE 1 (bases 1 to 18866)	AUTHORS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, M., Bryant, N.P., Bulay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavasca, S.R., Chen, G., Chen, G., Chen, Z., Chiu, D., Chowdhry, I. Christopoulos, C., Clen, G., D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C.,
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Elhaj, C., Emerling, S., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, M., Garza, M., Garza, M., Gall, R., Gorrell, J.H., Guevara, W., Gunarathe, P., Hale, S., Hamilton, K., Gorrell, J.H., Guevara, W., Gunarathe, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K., Hart, M., Havlak, P., Hales, S., Han, Harris, C., Harris, F., Howerd, S., Hober, J., Holloway, C., Hollins, B., Homsi, F., Jacobson, B., Jia, Y., Johnson, R., Mane, J., Korrah, J., Kovar, C., Karlson, E., Kelly, S., Khan, U., King, L., Korrah, J., Kovar, C., Lewis, L.C., Lewis, L.C., Loussey, E., Louse, R., Louse, R., Marchiner, E., Marchiner, E., Marchiner, E., Marchiner, R., Marchiner, R., Marchiner, R., Marchiner, E., Massey, E., Mawhiney, E., McLeod, M.P., Marchiner, E., Mitchell, T., Monabbat, K., Mongomery, K.T., Morgan, M., Morsen, M., Nguyen, N., Nguyen, N., Nguyen, D., Newson, J., Newtson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Parke, M., Paytor, R., Pacer, L., Peters, L., Pickens, R., Primus, E., Payton, B., Peery, J., Peters, L., Pickens, R., Painer, S., Robosheari, N., Sisson, I., Soott, G., Shen, H., Shora, M., Tang, H., Tangey, J., Tang, H., Tangey, J., Tang, H., Tangey, H., Stron, Y., Wallialon, S., Ward-Moore, S., Warren, R., Walleczyk, R., Wacherlapati, R., Walliagon, S., Williamson, R., Walliagon, S., Williamson, R., Walliagon, S., Walliamson, R., Walliagon, S., Walliamson, R., Walliagon, S., Walliams, G., Walliamson, R., Marliagol, S., Woller, R., Weinstock, G. and Gibbs, R., Thomas, S., Lower, R., Walliagon, S., Walliagon, S., Williams, S., Walliagon, R., Wa
```

Submitted (23-DEC-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 188666) 2 (bases 1 to 188666) Worley, K.C. Direct Submission Unpublished REFERENCE AUTHORS TITLE JOURNAL

Submitted (03-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Baylor Plaza, Houston, 4 (bases 1 to 188666) Direct Submission Worley, K.C AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE

Direct Submission Worley, K.C.

Submitted (23-APR-2002) Human Genome Sequencing Center, Department of Moliar and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 188666) Worley, K. AUTHORS TITLE JOURNAL REFERENCE

Direct Submission
Submitted (31-JUL-2002) Human Genome Sequencing Center, Department
Submitted (31-JUL-2002) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Oct 23, 2001 this sequence version replaced gi:16304255.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email

gc-help@bcm.tmc.edu

COMMENT

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences. ANNOTATION OF FEATURES: STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

repeat_region

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found

http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

QUALSTAT-REPORT.

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884. .2908
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786. .5959
Location/Qualifiers
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rpt_family="AluSp"
515. ,5550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpt_family="MLTLJ"
521. .6762
                                                                                                                                                                                                                                                                                                                                                                                                                                         761. .3999
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             . .188666
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                                                                                                       misc_feature
                    source
                                                                                                                                                                               STS
                                                                                                                                                 STS
   FEATURES
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Db 73136 GATTGGGTCAGCTAAATTGACTAAGTGTCTTTATCATTGATTTTTTACTACTACT 73077	9L 9L KÖ	Db 73076 TGAATGGCCTTGACAAGTTACAGGACTTCCATTGAATGTTAAAATTTCTTCTGTAAAAG 73017	97 7676 YO	Db 73016 GGAAATGGTAATACCTATCTTTTAATTATTGTAATAATTAAACAAGATAACAATTGGAAA 72957	2y 76 76	Db 72956 ACACCTAGGGACTTTCCAAGGGGCCTGTTACATGGCAAATGATCACCTTGGAATAGTGAG 72897	7676 YQ	Db 72896 TIGGGCICCCCCTGCIGITAAGAAACAGACTAGCGTAAGIGCGCAGGICTIGAITTCAIT 72837	7676 YQ	Db 72836 AGCTTTATTTTGGGCCATCTCCCTTAGATGAAAATTATTCTGTGAACTTTTGGCGG 72777	Qy 7676	Db 72776 GGGTTTGTTTTGAAACAGAGAATAATCATTAATTTATCAGATATTTATATAAAAGGGATT 72717	2y 76 76 VQ	Db 72716 TCTGACTCGGTGCGTAGAATGCTTACTATACAATTCTGCTGTTTGTCAAGTGTTCCTATA 72657	Qy 77	Db 72656 GITITITIAAAGGIAIGTIAACIAITITICCCITITIGGITIAIAITIGIAGGAAICITT 72597	Oy 78 AlaPheLySCysAlaArgAlaGluGluLeuPheAsnNetLeuGlnGlu1leMetGlnAsn 97		/2536 APINGIPIPARICIGGIGGARGAGCCAGIIGIAGARAGARAIAAICAICAGAAGAAIIG		RESULT 14 ALSB9661 LOCUS DEFINITION Mouse DNA sequence from clone RP23-58B7 on chromosome 15, complete	ACCESSION ALS89661 VERSION ALS89661.21 GI:18476659	Mus musculus (house mouse) SM Mus musculus	Euk? Mamm	Dunn, M. Direct Submission		humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk COMMENT On Feb 1, 2002 this sequence version replaced gi:18151481.	During sequence assembly data is compared from overlapping clo Where differences are found these are annotated as variations	together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission	corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.	This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate
	region		repeat_region 1015910228 /repeat_region /rpt_family="WLT2G" repeat_region complement(10511 10580)			repear_region iiiosiiiso /rpt_family="Alusg" //repear_region 11470			repear_region 11/26. 111905 /rpt_family="(GGAA)n" renear region complement(13137 19502)						repeat_region complement(15218. 15358) /rpt_family="MIR"	t_region	Alignment Scores: 3.03e-45 Length: 188666 Score: 452.00 Matches: 115 Percent Similarity: 31.27% Conservative: 1	Mismatches: Indels: Gaps:	US-09-757-415A-1_COPY_11_140 (1-130) x AC018921 (1-188666)	Oy 11 PheLysVallleAsnValAspAspAspGlyAsnGluLeuGlySerGly1leMetGluLeu 30	Oy 31 ThraspThrGluLeuIleLeuTyrThrargLysArgAspSerValLysTrpHisTyrLeu 50	51 CysLeuArgArgTyrGlyTyrAspSerAsnLeuPheSerPheGluSerGlyArgArgCys	DD /3435 IGCCIGCGACGALAIGACIAIGACIAGACIAIGA /35.70 OV 71 GluThrGlyGluGlyIle76	73375 CAAACTGGACAAGGTAG-AACCTTTGTTTTTTTCCCAAATATTGTATTG	yy 76767676	73316 TTTCAGCTATTCTGTATACAAAGATTAAATTAAIATTTTTCTTCTGAAAAAAAAAA	76	ATAAACAGATTGTTAAGGAAAGATATAGTATACTGTGTGTATTAATTTATCAACTGTTTATT	16	73196 AAGCACATTGTCTATGTGAGAAATTTTGGCTCATGTCAACTTTAAGATTTTTCAGTAAAT	Ογ 76 76

SOURCE

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misc_feature
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DB:
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                                                                                                                                            RETURN.

SE MINITYD, MARIE, Mezkew, Lee., Abranzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsprooks,S., Amin,A., Angulano,D.,
Allen,C., Allen,H., Alsprooks,S., Amin,A., Angulano,D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (13-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:23269032.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (12-JAN-2002) Human Genome Sequencing Center, Department
Submitted (12-JAN-2002) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 238379)
Rat Genome Sequencing Consortium.
                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Buteleostomi,
Mammalia, Eutheria; Rodentia, Sciurognathi, Muridae, Murinae,
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 238379)
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Unpublished
                                   Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Worley, K.C.
                                                                                                                                     Rattus.
                               ORGANISM
                                                                                                                                                             REFERENCE
AUTHORS
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REFERENCE
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JOURNAL
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JOURNAL
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in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shorgun sequence reads. Both end sequences and whole genome shorgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: Estimated insert size may differ from sequence length

(see http://www.ngsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* consists of 3 contigs. The true order of the pieces

is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 ValileasnValaspAspAspGlyAsnGluLeuGlySerGlyIleMetGluLeuThrAsp 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Consensus quality: 232564 bases at least Q40 consensus quality: 234634 bases at least Q30 Consensus quality: 236642 bases at least Q20 Estimated insert size: 246019; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235028 235127: contig of 235027 bp in length 235028 235127: gap of unknown length 235128 235231 contig of 1103 bp in length 236231 236330: gap of unknown length 236231 236330: gap of unknown length 236231 238379: contig of 2049 bp in length. Location/Qualifiers | /organism="Rattus norvegicus" /mol_type="genomic DNA" /mol_type="genomic DNA" /mol_type="genomic DNA" /clone="CH230-141M9"
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                                                                                                                                                                                                                                                           Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assembly program: Atlas 3.0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="wgs_end_extension
clone_end:T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         end sequence: BZ094321"
3203. .4009
/note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     end_sequence:BZ094321"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="clone_boundary
clone_end:T7_
site:EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone_end:T7
site:EcoRI
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62.69%
54.48%
48.78%
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Best Local Similarity:
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21057 GCAGGTAGAAGCAGGAGATTGTTGTAAATTCTACATAGCAAATTCCTGGCAAGGCCAGGG 21116
                                                                                               20937 GGACAAGGTAAGGTAAAGCCTTTATTTCTCCAGATGATACATATTCAAAGCACTGCACTTC 20996
20757 GTCATTAATGTGGATGACGATGGGAATGAGCTAGGCTCTGGTGTAATGGAGCTCACAGAC 20816
                                                                20817 ACGGAGCTGATTCTGTATACCCGGAAACGCGACTCGGTGAAGTGGCACTACCTCTGCCTA 20876
                                                                                                                                                                                                                                                        88 PheAsnMetLeuGlnGlulleMetGlnAsnAsnSerIleAsnValValGluGluProVal 107
                                                                                                                                                                                                                                  33 ThrGluLeuIleLeuTyrThrArgLysArgAspSerValLysTrpHisTyrLeuCysLeu 52
                                                                                                                                                                   22 ----- 75
                                                                                                                                                                                                                                                                                                                                                                                    ::::::|||
21117 TTABABAGGAAGACACTATGCCAATAAATACCACAGAAACT 21158
                                                                                                                                                                                                                                                                                                                                                                   -----HisGlnThr 115
                                                                                                                                                                     73 GlyGlnGly-------
                                                                                                                                                                                                                                                                                                                                                                 108 ValGluArgAsnAsn----
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Search completed: August 8, 2004, 23:07:18 Job time : 4938.38 secs

Human pro EST clone EST clone Haematopo Human pol Human pol Novel hum Human NoVel

Aav89905

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ALIGNMENTS
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AAH32551
ACH47613
AAF65334
ACH37206
AAH34891
                                                                                                                                               ABZ73594
ADA98101
ADA43970
        AAV89905
AAZ94091
                AAZ94125
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AA15806748
AA158062
ADB48944
ACF06235
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AABA8963
AABA8963
                                                                  AAI59684
AAI57898
                                                                               AAH14202
AAI60736
                                                                                                                                  AAK58197
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                                                                           ADD71184
                                                                                                                                                                                     ADC35143 standard; cDNA; 1532
                                                                                                                                                                                                      18-DEC-2003 (first entry)
ADC35143;
                                                                                                                                                                                  ADC35143
 RESULT
                                                                                                                                                                                      υ
                                                                                                                                       8, 2004, 19:43:05; Search time 513.158 Seconds (without alignments) 1076.210 Million cell updates/sec
                                               US-09-757-415A-1_COPY_11_140 696
1 DIVPDNHRNKFKVINVDDDG......NNHQTELEVPRIPRIPTIFG 130
     GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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                                                                                                  Potal number of hits satisfying chosen parameters:
                                                                                          3373863 segs, 2124099041 residues
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Maximum Match 100%
Listing first 45 summaries
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0.05
0.05
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Xgapop 10.0 , Xgapext 0
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Delop 6.0 , Delext 7
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                                                 score
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Minimum DB Maximum DB

Scoring table:

Sequence: Title: Perfect

OM protein

on:

Run

Bosinophi Drosophil Human pol Human sec Human sec Human col Human col Human sec Human sec

Aaz94091 F
Aai594125 F
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Adb48943 I
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Abi10803 I
Abi10803

Diagnosing breast cancer in subject by obtaining biological sample from subject, contacting sample with breast cancer-associated polypeptides, determining specific binding between polypeptides and agents in sample. breast cancer; breast cancer diagnosis; breast cancer antigen; gene; ss. Chen Y; Human breast cancer antigen polynucleotide seq id 27. Gure A, old LJ, Scanlan MJ, Gout I, Stockert E, (LUDW-) LUDWIG INST CANCER RES. L5-MAY-2002; 2002US-00146473. 15-MAY-2001; 2001US-0291150P. WPI; 2003-829397/77. P-PSDB; ADC35101 US2003108888-A1. Homo sapiens. 12-JUN-2003.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

П

DB

Query Match Length

Score

No.

Result

Adc35143 Human bre Aba09066 Human FGF Aax39606 Breast ca Ach40178 Human foe Ab122607 Drosophil Ab122606 Prosophil Aav38415 DNA encod Add14695 Human src

ADC35143 ABA09066 AAX39606 ACH40178 ABL22607 ABL22607 AAV38415 ADD14695

1532 2074 766 452 1329 3329 1446

1000.0 1700.0 74.4 38.0 255.0 20.6 20.6

696 696 517.5 264.5 174 174 143.5

12545050

Description

SEQ ID NO 27; 173pp; English.

The invention describes a method of diagnosing breast cancer in subject comprising contacting biological sample from subject with at least two different breast cancer-associated polypeptides (I) encoded by nucleic acid molecules (II) comprising sequence chosen from 42 fully defined sequences as given in specification, determining specific binding between (I) and agents in sample, where presence of the binding is diagnostic for breast cancer. The method is useful for diagnosing breast cancer in a subject. The sequence encodes a breast cancer in a first sequence encodes a breast cancer antigen.

Sequence 1532 BP; 501 A; 333 C; 339 G; 359 T; 0 U; 0 Other; Length: Matches: Conservative: Mismatches: Indels: 2.23e-82 696.00 100.00% 100.00% Local Similarity: Percent Similarity: Alignment Scores: Query Match: DB: .. ON

US-09-757-415A-1_COPY_11_140 (1-130) x ADC35143 (1-1532)

155 101 AsnValValGluGluFroValValGluArgAsnAsnHisGlnThrGluLeuGluValPro 120 156 AAACGTGACTCAGTAAAATGGCACTACCTCTGCCTGCGACGCTATGGCTATGACTCGAAT 215 Crcritircriticaaaacregiceaagerereaacregacaagearcritigecritiaag 275 81 CysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGluIleMetGlnAsnAsnSerIle 100 395 50 95 40 LysArgAspSerValLysTrpHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsn 60 80 1 AspThrValProAspAsnHisArgAsnLysPheLysValIleAsnValAspAspGly GACACTGTCCCAGATAACCATCGGAACAAGTTTAAGGTCATTAATGTGGATGATGATGGG AsnGluLeuGlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArg 96 AATGAGTTAGGTTCTGGCATAATGGAACTTACAGACAGAGAACTGATTTTATACACCCGC LeuPheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePheAlaPheLys 336 AAIGIGGIGGAAGAGCCAGIIGIAGAAAGAAAIAAICAICAGACIGGAAGICCCI AGAACACCTCGAACACCTACAACTCCAGGA 425 ArgihrProArgihrProThrihrProGly 130 41 61 216 121 396 ò d à g ò 셤 à g 임 임 ò g ò à

ABA09066 standard; cDNA; 2074 RESULT

ABA09066;

11-JAN-2002 (first entry)

Human FGFR signalling adaptor SNT-1 homologue cDNA, SEQ ID NO:842.

Human; cytokine; cell proliferation; cell differentiation; growth, hemacropoiesis regulation; tissue growth; immunomodilator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; thrombolysis; oncogenesis; proliferation; metastasis; cancer; throur; haemacopoietic disorder; meloid cell disorder; asthma; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; osteoporosis; vascular growth disorder; cancer accenting; drug screening; gene therapy; antiinflammatory; ABA09066
XX
AC ABAC
XX
DT 11-c
XX
DT 11-c
XX
DE Hum
XX
DE Hum
XX
DE Hum
XX
CM inh
CM inh
XW gro
XW chr

antiasthmatic, antiarthritic, haemostatic, antiarteriosclerotic, cytostatic, osteopathic, vasotropic, cardiant, virucide, antibacterial, antifungal; vulnerary, antiulcer; ss.

Homo sapiens.

WO200157188-A2.

09-AUG-2001.

05-FEB-2001; 2001WO-US003800.

03-FEB-2000; 2000US-00496914. 27-APR-2000; 2000US-00560875.

(HYSE-) HYSEQ INC.

Fang YT, Liu C, Drmanac RT;

WPI; 2001-457740/49. P-PSDB; ABB11822 Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer

Claim 1; Page 748; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA0925-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant bost cells comprising a nucleotide of the invention, methods of producing the nucleotides.

CC antibodies against the polypeptides, methods of deethifying compounds which bind to polypeptides in a sample, and methods of identifying compounds which prolypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence cc pipeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence cc potential therapeutic applications. The polypeptides of the invention may have various activities; send cell growth factor activity;

GIVING AND AND ACTIVITY, activity issue growth activity;

Immunomodulatory activities; receptor or ligand activities; or chemokinetic activities, has presented activities, or bemokinetic activities, neceptor or ligand activities or thrombolytic activities, receptor or ligand activities of the invention are useful for preventing, treating or anelorating medical conditions, e.g., by protein or gene therapy. Such conditions include and anormal activity and properties and inflammatory conditions (e.g., asthma or arthritis), arterial ischaemia, bone disorders (e.g., asthma or arthritis), arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal configurating (e.g., of burns, incisions and ulcers), while those with challed and funding cell and promote wound changed in growth, factor activity may be used to promote wound changed with growth factor activity may be used to promote wound configure activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disease or actidental damage. The presente sequence of promote cell growth factor activity may be used in the diagnosis of the above conditions, and indiance and nev novel human polypeptide of the invention

Sequence 2074 BP; 634 A; 478 C; 491 G; 471 T; 0 U; 0 Other;

Length: Matches: Conservative: Mismatches: 3.43e-82 696.00 100.00% 100.00% Percent Similarity: Best Local Similarity:

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ss; sequencing by hybridisation; SBH; expressed sequence tag; mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 Gluvalpro---ArgThrProArgThrProThrPro 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGTCCCTAANAACAACCTCGAAACAACTACAACTCCA 757
                                                                                                                                                                                                                                                                            US-09-757-415A-1_COPY_11_140 (1-130) x AAX39606 (1-766)
                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Page 375; 787pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human foetal brain cDNA #1545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACH40178 standard; cDNA; 452
                                                                                                                                                                                                       5.33e-59
517.50
87.77%
86.33%
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Best Local Similarity:
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                                                                                                                                                                           Sequence 766
                                                                                                                                                                                              Alignment Scores:
Pred. No.:
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                                                                                                                                                         lung cancer
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ACH40178
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                                                                                                                                                                                                CICITITICITITICAAAGIGGICGAAGGIGICAAACIGGACAAGGAAICITIGCCITIAAG 814
                                                                                                                                                                                                                   CysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGluIleMetGlnAsnAsnSerIle 100
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                                                                                                                                    LysArgAspSerValLysTrpHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsn 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Cancer associated antigen; diagnosis; research; treatment; human;
breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
prostate cancer; ss.
                                                                                                                                                                                                                                 TGTGCCCCGTGCAGAAGAATTATTTAACATGTTGCAAGAGATTATGCAAAATAATAATATATA
                                                                                                          GACACTGTCCCAGATAACCATCGGAACAAGTTTAAGGTCATTAATGTGGATGATGATGGG
                                                                                              AsnGluLeuGlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArg
                                                                                                                                                                            LeupheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePheAlaPheLys
                                                     AspThrValProAspAsnHisArgAsnLysPheLysVallleAsnValAspAspAspGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen Y, Gout
O, Sahin U;
                                 US-09-757-415A-1_COPY_11_140 (1-130) x ABA09066 (1-2074)
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1, Tureci O,
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Pfreundschuh M,
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97US-0061599P.
97US-0061765P.
97US-00948705.
97GB-00021697.
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     100.00%
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, Obata Y,
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11-OCT-1997;
22-JUN-1998;
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The invention relates to a method for diagnosing a disorder characterised by expression of a human cancer associated antigen precursor coded for by a mucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in the diagnosis, monitoring, research, or treatment of conditions. The invention provides nucleic acid sequences and encoded polypeptides which are cancer associated antigen precursors expressed in human breast cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         359 GACACTGTCCCAGATAACCATCGGAACAAGTTTAAGGTCATTAATGTGGATGATGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ASPThrValProAspAsnHisArgAsnLysPheLysVallleAsnValAspAspGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP; 251 A; 151 C; 173 G; 190 T; 0 U; 1 Other;
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478

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538

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598

117

658

(first entry)

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101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones LW;
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 452 BP; 98 A; 152 C; 108 G; 93 T; 0 U; 1 Other;
                                                                                                                          Dickson MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-757-415A-1_COPY_11_140 (1-130) x ACH40178 (1-452)
                                                                                                                                                                                                                                                                                                                                                                                  seqdata.uspto.gov/sequence.html?DocID=20030073623
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                           Claim 1; SEQ ID NO 27390; 44pp; English.
                                                                                                                         Stache-Crain B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
ABL22607
ID ABL22607 standard; DNA; 1329 BP.
                            30-JUL-2001; 2001US-00918995.
                                              30-JUL-2001; 2001US-00918995.
                                                                                                                                                                                                                                                                                                                                                                                                                             1.39e-25
264.50
84.72$
68.06$
                                                                           LABAT I.
STACHE-CRAIN B.
                                                                                                                        Drmanac RT, Labat I,
                                                                                            DICKSON M C.
JONES L W.
                                                                 DRMANAC R T.
                                                                                                                                           WPI; 2003-615964/58
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                         (LABA/) (STAC/) (DICK/) (JONE/)
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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                          Drosophila melanogaster genomic polynucleotide SEQ ID NO 19294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 19294; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                    33-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                  Drosophila melanogaster
                                                                                                                                                                           pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                              WO200171042-A2
                                                              26-MAR-2002
                                                                                                                                                                                                                                                                                                          27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter JC,
                       ABL22607;
The invention relates to an isolated polymucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polymucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (BST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is one of the 38043 isolated cDNA/BST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was constant and an electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                  New polymucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.
                17-APR-2003
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Myers EW;

Li PWD,

13 225 226 TCCTTCGAAGCAGGACGTAGGTGTATGTCTGGGCCAGGGATCTACACGTTTCGAGTCCAC 285 42 62 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-AB130511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB27373-ABB72072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences 7 HisArgAsnLysPheLysVal-----IleAsnValAspAspAspGlyAsnGlu 23 LeuGlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArgLysArg SerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePheAlaPheLysCysAla 43 AspSerValLysTrpHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsnLeuPhe GAGCCCATTGTCTGGGCACTGCAACACCTCCGACGTTATGGGTTGAATAACGATCTTTC Sequence 1329 BP; 320 A; 385 C; 346 G; 278 T; 0 U; 0 Other; x ABL22607 (1-1329) Conservative: Mismatches: Indels: Matches: Length: US-09-757-415A-1_COPY_11_140 (1-130) 7.516-13 174.00 52.46% 34.43% 25.00% Percent Similarity: Best Local Similarity: Alignment Scores: 63 Query Match: ò g δ g à d ò g

161

66

83 ArgAlaGluGluLeuPheAsnMetLeuGlnGluIleMetGlnAsnAsnSerIleAsnVal 102

SerpheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePheAlaPheLysCysAla

63

43 AspSerValLysTrpHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsnLeuPhe

LeuGlySerGlylleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArgLysArg 42

23

2044 AATGCCGAGCAGCAGCTGTATCCGATGTTTCAGCGCTACATCAACGCGGTGAATACAGATGCC 1985

83 ArgAlaGluGluLeuPheAsnMetLeuGlnGluIleMetGlnAsnAsnSerIleAsnVal 102

1984 ITTGTGCAGGGCGAACGAGAAAGGGTTAACTCCGCTCATTCGGTGTCCGTAAATATGGGC 1925

ΒЪ.

AAV38415 standard; DNA; 1446

AAV38415;

1924 CGTACT 1919

121 ArgThr 122

103 ValGluGluProValValGluArgAsnAsn-----HisGlnThrGluLeuGluValPro 120

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AAV38415
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 103 ValGluGluProValValGluArgAsnAsn-----HisGlnThrGluLeuGluValPro 120
                                                             405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                      346 TITGIGCAGGGCGAACGAGAAGGGITAACICCGCTCAFTCGGTGICCGTAATAIGGGC
                                                                                                                                                                                                                                                                   developmental biology; cell signalling; insecticide
                                                                                                                                                                                                                                           melanogaster genomic polynucleotide SEQ ID NO 19291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 19291; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3329 BP; 880 A; 746 C; 747 G; 956 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                   ABL22606 standard; DNA; 3329 BP
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11-JUL-2000; 2000US-00614150.
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(first entry)
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                                                                                                                                                                                                                                                                                     pharmaceutical; gene; ds
                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-656860/75.
                                                                                                                 411
                                                                                        ArgThr 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PEKE ) PE CORP NY.
                                                                                                                  CGTACT
                                                                                                                                                                                                                                                                                                                                       WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interactions.
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                                                                                                                                                                                                                                                                         Drosophila;
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                                                                                                                                                                                                                                                 Drosophila
                                                                                                                                                                                            ABL22606;
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The present sequence encodes p62-dok (protein downstream of tyrosine kinases) protein. The protein is tyrosine phosphorylated in haematopoieic
                                                                                                                                                                                                                                                                                                                                                                                                                     develop products for the oncogenic tyrosine kinase
                                                                                       tyrosine phosphorylation; receptor tyrosine kinase; oncogenic cell; pl20 ras GTPase-activating protein; GAP; signal transduction pathway; antibody; diagnosis; treatment; chronic myelogenous leukaemia; CML;
                                                                                                                                                                                                                                                                                                                                                                BD;
                                                          DNA encoding p62 protein downstream of tyrosine kinases (p62-dok)
                                                                                                                                                                                                                                                                                                                                                                Clarkson
                                                                                                                                                                                                                                                                                                                                                                 Strife AO,
                                                                               protein downstream of tyrosine kinases;
                                                                                                                                                                                                                                                                                                                                                                                                                     Newly isolated human p62-dok protein - used to diagnosis and treatment of conditions in which is active, e.g. chronic myelogenous leukaemia.
                                                                                                                                                                                                                                                                                                                                                                 Wisniewski DG,
                                                                                                                                                                                                                                                                                                                                 COLD SPRING HARBOR LAB.
SLOAN KETTERING INST CANCER RES
                                                                                                                                                                       Location/Qualifiers
1. 1446
/*tag= a
/product= "p62-dok"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 2A-C; 86pp; English.
                                                                                                                                                                                                                                                                                                96US-0030418P.
                                                                                                                                                                                                                                                                           97WO-US019788
                                                                                                                                                                                                                                                                                                                                                                  α,
                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                  Kobayashi
                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-286945/25.
P-PSDB; AAW62507.
                                                                                                                              human cancer;
                                                                                                                                                                                                                                                                           30-OCT-1997;
                                                                                                                                                                                                                                                                                                01-NOV-1996;
22-JAN-1997;
                                                                                                                                                                                                                                 WO9820129-A1
                                                                                                                                                                                                                                                                                                                                                                   NA,
                                        16-SEP-1998
                                                                                                                                                                                                                                                      14-MAY-1998
                                                                                 p62-dok; |
tyrosine |
                                                                                                                                                    Mammalia
                                                                                                                                                                                                                                                                                                                                 (COLD-)
                                                                                                                                                                                                                                                                                                                                                                    Carpino
                                                                                                                                                                          Key
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HisArgAsnLysPheLysVal-----IleAsnValAspAspGlyAsnGlu 22

(1-3329)

US-09-757-415A-1_COPY_11_140 (1-130) x ABL22606

 δ ద

3329 222 22 6 6 7

2.76e-12

174.00 52.46% 34.43% 25.00%

Similarity:

Percent Similarity: Best Local Similari

Best Local S. Query Match:

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mammalian cells after stimulation with a ligand for a receptor tyrosine kinase found in oncogenic cells. The p62-dok protein binds p120 ras GTPase-activating protein (GAP). The p62-dok protein is involved in a signal transduction pathway initiated by receptor tyrosine kinase, and is rapidly tyrosine phosphorylated. The p62-dok protein is also present in romal cells, but is not constitutevily phosphorylated by normal receptor tyrosine kinase. Antibodies against p62-dok and aberrantly phosphorylated p62-dok, and probes derived from the p62-dok and aberrantly phosphorylated p62-dok, and probes derived from the p62-dok bNA sequence can be used in the diagnosis and treatment of conditions in which an oncogenic tyrosine
                                                                                                                                                                                                                                                                                                                    kinase is active such as chronic myelogenous leukaemia (CML) and other
                                                                                                                                                                                                                                                                                                                                                        human cancers
       8.866666666668888
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ucleotides and polypeptides for predicting the activity of that interact with protein tyrosine kinases and/or protein

Claim 2; SEQ ID NO 89; 139pp; English.

tyrosine kinase pathways.

New polynucleotides and

Shaw

Lee

GR,

Fairchild

E

WPI; 2003-636735/60

P-PSDB; ADD14099.

Sequence 1446 BP; 285 A; 457 C; 440 G; 264 T; 0 U; 0 Other;

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514 GGCTCCTACGTGCTGAGGGTGGAGGCTGAAAGGCTGACTCTCCTGACCGTGGGGGCCCAG 573
                                                                                                                                                                                                                                    633
                                                                                                                                                                                                                                                                                           693
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                                                                                                                                                                                                                                                              11
                                                                                                                                         GlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArgLysArgAsp 43
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                                                                                                                                                                                                                      694 ACCTICCAGACGGCACAGGGAAAIGACAICTICCAGGCAGIIGAGACIGCCAICCACCGG
                                                                                                                                                                                                      ------ValLysTrpHisTyrLeuCysLeuArgArgTyrGlyTyr
                                                                                                                                                                                                                                                            AspSerAsnLeupheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGly1lePhe
                                                                                                                                                                                                                                                                                        534 GACAAGGTCATGTTCTTTTCGAGGCCGGCCGCCGCTGCCCTCAGGCCCTGGAACCTTC
                                                                                                                                                                                                                                                                                                                   78 AlaPheLysCysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGluIleMetGlnAsn
               1446
33
20
50
9
                                                                                                              US-09-757-415A-1_COPY_11_140 (1-130) x AAV38415 (1-1446)
                          Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              814 GGGGAGGTGGCAGAGGGGAAGTTGCCTTCCCCACCT
               Length:
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                9.88e-09
                      143.50
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20.62%
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Alignment Scores:
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predictor set; protein tyrosine kinase activity modulator; protein tyrosine kinase; oytostatic; gene therapy; drug sensitivity; genetic profile; cancer; human; gene;
                                                                     Human src biomarker polynucleotide SEQ ID NO:89.
                 ADD14695 standard; cDNA; 1972 BP
                                                   (first entry)
                                                   01-JAN-2004
                                                                                                                         Homo sapiens
                                  ADD14695;
       RESULT
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The present invention describes a predictor set comprising a plurality of polynucleotides or polypeptides whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein tyrosine kinase activity or members of the protein tyrosine kinase activity or members of the protein tyrosine kinase protein tyrosine kinase activity of cells, comprising obtaining a sample of cells, comprising obtaining a sample of cells, comprising obtaining a sample of cells, controlled the activity of the cells, comprising obtaining whether the cells express a plurality of markers, and correlate the activity of the cells, [2] a plurality of markers, and correlate with compound sensitivity or resistance of cells associated with a disease state, and [3] identifying polynucleotides and cells associated with a disease state, comprising subjecting the plurality of associated with a disease state, comprising subjecting the plurality or cell lines to one or more compounds, analysing the expression pattern of a microarray of polynucleotides that predict the sensitivity or cesistance of cells associated with a disease state by using the compounds that predict the sensitivity or cesistance of cells associated with a disease state by using the correstive pattern of the microarray. The polynucleotides and certain pattern of the microarray. The polynucleotides and certain tyrosine kinase pathways. These may be used in determining drug certainity of compounds that interact with protein tyrosine kinase pathways. These may be used in dividualized carrity by center profiles which aid in treating diseases and disorders (e.g. center) based on patient response at a molecular level. The present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              720 GACAAGGTCATGTÍCÍTÍTÍTCGAGGCCGGCCGCCGCTGCCCTCAGGCCCTGGAACCTÍC 779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 AlapheLysCysAlaArgAlaGluLeuPheAsnMetLeuGlnGluIleMetGlnAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 AspSerAsnLeuPheSerPheGluSerGlyArgArgArgCysGlnThrGlyGlnGlyIlePhe
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83

(BRIM) BRISTOL-MYERS SQUIBB CO. 18-JAN-2002; 2002US-0350061P. 17-JAN-2003; 2003WO-US001981

WO2003062395-A2

31-JUL-2003

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Human, ss, gene, prostate specific nucleic acid, cytostatic, PSNA, prostate cancer, gene therapy, vaccine, non-cancerous prostatic disease.
                                                                                                                                                                                                                                     New prostate specific polypeptides useful for identifying, diagnosing, monitoring, staging, imaging and treating prostate cancer and non-cancerous disease states in prostate.
900 GGGGAGGTGGCAGAGGAGGAAGTTGCCTACCCACCT 935
                                                                                Human prostate specific gene sequence DEX0283_68,
                                                                                                                                                                                                            Sun Y,
                                                                                                                                                                                                                                                                       Claim 1; Page 179-181; 248pp; English
                                                                                                                                                                                                             Recipon H,
                                      ABK95303 standard; cDNA; 3809
                                                                                                                                                                 20-NOV-2001; 2001WO-US045177.
                                                                                                                                                                               21-NOV-2000; 2000US-0252189P.
                                                                  (first entry)
                                                                                                                                                                                                             Macina RA,
                                                                                                                                                                                               (DIAD-) DIADEXUS INC
                                                                                                                                                                                                                           WPI; 2002-500278/53.
                                                                                                                                     WO200242329-A2
                                                                                                                      Homo sapiens
                                                                   24-SEP-2002
                                                                                                                                                   30-MAY-2002
                                                                                                                                                                                                              Salceda S,
                                                     ABK95303;
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Liu C;

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The invention relates to an isolated polypeptide that comprises a sequence with 60 % sequence identity to one of 103 prostate specific colory polypeptide (PSP) sequences (S1), given in specification, or a sequence concoded by a nucleic acid comprising one of 114 prostate specific nucleic acid (PSNA) sequences (S2), given in specification. Also included are a cord comprising the PSNA, a host cell comprising the vector.

CC acid (PSNA) sequences (S2), given in specification. Also included are a preparation of the PSP, a polypeptide encoded by the PSNA; an anti-PSP cantibody the antibody or its fragment, a kit for detecting a risk of cancer in a patient, comprising a unit for and a vaccine comprising the PSP or the PSNA, The PSNA; a seaple of a patient of a prostate specific nucleic acid (PSNA) in a sample. The antibody to the PSP or the PSNA, The PSNA is useful for amplied the presence of a prostate specific nucleic acid (PSNA) in a cample. The antibody to the PSP is useful for determining the presence of a prostate cancer, where the administration of the antibody induces an immune response against the prostate cancer cell antibody induces an immune response against the prostate cancer in a patient. The PSP is useful as a vaccine component of relating a humoral and/or cellular immune response, and for prostate cancer in a patient. The PSP is useful as a vaccine component of conting transgenic animals and cells, and for producing transgenic animals and cells, and for producing ransgenic animals and cells, and for producing prostate cancer by detecting genetic lessons or mutations. The PSP and the PSNA is useful for staging and prostate cancer. The PSP and the PSNA are also useful for staging and prostate tissue and the antibody are useful for identifying prostate tissue and the antibody are useful in dispensing and prostate cancer. The PSP and the PSNA are also useful for identifying prostate tissue and the antibody are useful. The PSP and the PSNA are useful and and an entering and the antibody are useful and tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosing, monitoring, staging, imaging and treating prostate cancer and non-cancerous disease states in prostate tissue. The present sequence is a prostate specific nucleic acid (PSNA) sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    925 A; 1003 C; 1167 G; 714 T; 0 U; 0 Other;
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||||:::|||:::|||2637 CAGAAAGGCCGGACAGGCACGATGTTCTCAGAGCTGACTCCCATGAA 2696
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                                                                                                                                                  present sequence represents a human expressed sequence tag (EST). The
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                                                                                                                                                                                                                                 77
                                                                                                                                                                                                                                                                                   78 AlaPheLysCysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGluIleMetGlnAsn 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries.
                                                                                                                           GlyserGly1leMetGluLeuThrAspThrGluLeu1leLeuTyrThrArgLy8ArgAsp 43
                                                                                                                                                                                               2457 AGTCAGATACTGGAGCCACTCCTGTCCTGGCCCTACACTCTGTTGCGTCGCTATGGCCGG
                                                                                                                                                                                                                                 AspSerAsnLeuPheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePhe
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                                                                                                US-09-757-415A-1_COPY_11_140 (1-130) x ABK95303 (1-3809)
                                                                                                                                                                                                                                                                                                                                                                                                                     2697 GGGGAGGTGGCAGAGGAGGTTGCCTTCCCCACCT 2732
                                                                                                                                                                                                                                                                                                                                                                                              115 ThrGlubeuGluValProArgThrProArgThrPro 126
                                     Conservative:
                                               Mismatches:
Indels:
         Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV89621 standard; cDNA; 205
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        3.9e-08
143.50
47.32%
29.46%
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Spaulding V, Agostino MJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                     Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST clone CO474.
                                                                                                                                                                                   44 Ser----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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Alignment Scores:
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polymucleotide, which is a secreted BST, and the encoded protein are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activity, chemocactic/chemokinatic activity, haemostatic and thrombolyvic activity, receptor/ligand activity, haemostatic and thrombolyvic activity, receptor/ligand activity, inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The polymucleotide may also be useful for
                                                                                                                                                                                                                                                                                                                       gene therapy
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53 A; 30 C; 40 G; 82 T; 0 U; 0 Other; Sequence 205 BP;

Alignment Scores:

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113 GGAATCTTTGCCTTTAAGTGTGCCCGTGCAGAAGAATTATTTAACATGTTGCAAGAGATT 172
                                                                                                                            GlyIlePheAlaPheLysCysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGluIle
                                                                                                   x AAV89621 (1-205)
  Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                  MetGlnAsnAsnSerIleAsnVal 102
                                                                                                 US-09-757-415A-1_COPY_11_140 (1-130)
9.82e-10
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Best Local Similarity:
Query Match:
DB:
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ATGCAAAATAATAGTATAAATGTG 196 173 셤

AAV89905 standard; cDNA; 205 AAV89905 RESULT 11 AAV89905

BP.

15-FEB-1999 (first entry)

EST clone CT474.

Human, secreted protein, expressed sequence tag, EST; haematopoiesis, tissue growth, activin, inhibin, chemotaxis, chemokinesis, haemostatic, receptor, ligand, thrombolytic, anti-inflammatory, cadherin, anti-tumour, gene therapy; ss

WO9845436-A2

15-OCT-1998

98WO-US006955 10-APR-1998;

97US-00838821, 10-APR-1997;

(GEMY) GENETICS INST INC

Jacobs K, Mcc Spaulding V,

New polynucleotides encoding human secreted proteins - derived from human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries. WPI; 1999-070077/06.

Φ. Ω

Treacy

Merberg D,

Mccoy JM, Lavallie ER, Racie LA, /, Agostino MJ;

Claim 1; Page 368; 618pp; English.

The The present sequence represents a human expressed sequence tag (EST). polynucleotide, which is a secreted EST, and the encoded protein are predicted to have useful biological activities which would make them

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113 GGAATCTTTGCCTTTAAGTGTGCCCGTGCAGAAGAATTATTTAACATGTTGCAAGAGATT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of nucleic acid SA61 isolated from mouse primitive stem cells by methods of the invention. It is an example of claimed isolated nucleic acids (see AAZ94077-Z9413) that are specifically expressed in hematopoietic stem cells (HSCS) and which encode HSC-specific proteins. The HSCs are especially primitive HSCs (PHSCS) such as umbilical cord cells, bone marrow cells and foetal liver cells. The encoded proteins (see AAY9176-93) are growth factors, transcription factors, splicing factors, capping factors, transport proteins, translation factors or replication factors that modulate HSC
suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haemetopolesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/chemokinetic activity, haemetostatic and thrombolytic activity, eceptor/ligand activity, anti-inflammatory activity, cabherin/tumour invasion suppressor activity, tumour inhibition activity. The polynucleotide may also be useful for
                                                                                                                                                                                                                                                                                                                                                                              GlyIlePheAlaPheLysCysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGluIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hematopoletic stem cell signaling proteins modulating replication and differentiation for treating immune system disorders and leukemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SA61; haematopoietic stem cell; immune system disorder; leukaemia; antileukaemic; immunomodulator; therapy; mouse; ss.
                                                                                                                                                                      G; 82 T; 0 U; 0 Other;
                                                                                                                                                                                                                        Haematopoietic stem cell specific nucleic acid SA61.
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Matches:
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                                                                                                                                                                                                                                                       Percent Similarity:
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activity, especially differentiation or replication. The invention provides a claimed method for identifying PHSC-specific nuclaic acids involving: creating a PHSC conal library and a non-PHSC immune cell library; and subtracting the 2 libraries. Also claimed are methods: for generating a stem cell/progenitor cell from PHSCs; for identifying the presence of a PHSC in a sample; for identifying the presence of a compound that modulates HSC activity; for using such a compound to treat an immune system condition, especially leukaemia; for introducing exogenous nucleic acid into a HSC; and for ex vivo expansion of HSCs. Also claimed is a PHSC specifically expressing 1 of the claimed nucleic
                                                                                                                                                                                                                                                                                                                                              LeuGlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArgLysArg 42
                                                                                                                                                                                                                                                                                                                                                                                                       AspSerValLysTrpHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsnLeuPhe
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The present sequence is that of a nucleic acid isolated from mouse primitive stem cells by a method of the invention. It is an example of claimed isolated nucleic acids (see AA294077-294131) that are example of specifically expressed in haematopoietic stem cells (HSCs) and which encode HSC specific proteins. The HSCs are especially primitive HSCs (PHSCs) such as umbilical cord cells, bone marrow cells and foetal liver cells. The encoded proteins (see AA79176-93) are growth factors, transport proteins, translation factors or replication factors, transport proteins, translation factors or replication. The invention provides a claimed method for identifying PHSC specific nucleic acids involving: creating a PHSC cDNA library and a non-PHSC immune cell involving: creating a PHSC cDNA library and a non-PHSC immune cell presence of a PHSC in a sample companied method for identifying PHSCs; for identifying the presence of a PHSC in a sample companied that modulates HSC activity; for using such a compound to treat an immune system condition, especially leukaemia; for introducing exceptous nucleic acid into a HSC; and for ex vivo expansion of HSCs. All and a chaimed mucleic acid into a HSC; and for ex vivo expansion of HSCs. All and a chaimed mucleic acid into a HSC; and for ex vivo expansion of HSCs.
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                                                                                                                                                                                                                                                  Hematopoietic stem cell signaling proteins modulating replication and differentiation for treating immune system disorders and leukemia.
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Matches:
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Gaps:
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Best Local Similarity:
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                                                                                                                                                              Lemischka I,
                                                                                     21-AUG-1998;
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                 02-MAR-2000
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Liu C, Asundi V, Chen R,
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                             4.36e-08
137.50
49.07%
31.48%
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21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
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19-JUL-2000; 2000US-00620312.
03-AUG-2000; 2000US-00653450.
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2000US-00693036
2000US-00727344
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                                                                   Percent Similarity:
Best Local Similarity:
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                     Alignment Scores:
Pred. No.:
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                                                                                                       Query Match
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||||||||| GAGCCCCTGGAGAGGTTGGGGCCCCAGATTTGAGCTGCCACTCCCAGAAAG 1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang D;
, Zhao QA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acids and polypeptides, useful for treating disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention relates to human nucleic acids (AAI57798-AAI61369) and the
                                                                                                                                                                                                                                                                                          Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancerperipheral nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chrombolytic; drug screening; arthritis; inflammation;
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Yang Y,
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Xue AJ,
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Wang Z, Wehrman T, Xu C,
Goodrich R, Drmanac RT;
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                                                125 ThrPro---ThrThrProGly 130
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                                                                                                                                                      AAI60749 standard; cDNA; 1123 BP.
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                                                                                   1016 CTGCCTCTAACTGATCCCGGG
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2000US-00488725.
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2000US-00598042.
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2000US-00662191.
2000US-00693036.
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AAI60749
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829
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                                                                                                                                                                                                                                                                                                                                          44 SerValLys-----TrpHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsn
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                                                    Conservative:
Mismatches:
Indels:
  Length:
Matches:
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Zhao QA;
   Yang Y, Zhang J,
Wang Z, Wehrman T, Xu C, Xue AJ, Goodrich R, Drmanac RT;
                                              WPI; 2001-442253/47.
P-PSDB; AAM41592.
    Wang J,
Zhou P,
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Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.

Claim 1; SEQ ID NO 4737; 10078pp; English.

The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic acitvity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous injuries, peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic collisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemoreatic/chemokinetic activity, haemostatic and thrombolyvic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification

Alignment Scores: Pred. No.:	4.36e-08	Length:	1123
Secore: Percent Similarity: Best Local Similarity: Query Match: DB:	1557.00 11.488 11.488 10.768	Marches: Conservative: Mismatches: Indels: Gaps:	11416 1006

US-09-757-415A-1_COPY_11_140 (1-130) x AAI60748 (1-1123)

δ	24 GlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArgLysArgAsp 43
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ò	44 SerValLysTrpHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsn 60
Db	602 AAGGTCAAACTGGTGATGTGGCCTCTCAGCTCACTGAGGAGATACGGTCGGAACTCAACG 661
ζ	61 LeuPheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePheAlaPheLys 80
Dp	AGGAAGAATGTGACACAGGAGAAGGACTATTCACTT
ζŏ	81 CysalaArgAlaGluGluLeuPheAsnMetLeuGlnGluIleMetGlnAsnAsnSerIle 100
Db	722 ACAAGGGAAGGAGAAATGATCTATCAGAAGGTTCATTCTGCGACACTG 769
ò	101 AsnValValGluGlu
qq	770 GCCATAGCTGAGCAACATGAAAGATTAATGCTAGAAATGGAACAGAAGGCCCGGCTTCAG 829
δy	115 ThrGluLeuGluValProArgThr 122
Dp	830 ACAGCTIGACTGAACCAATGACA 853

Search completed: August 8, 2004, 21:31:31 Job time : 524.158 secs

- nucleic search, using frame_plus_p2n model

OM protein

August 8, 2004, 21:03:30 ; Search time 3606.64 Seconds (without alignments) 1076.370 Million cell updates/sec Run on:

US-09-757-415A-1_COPY_11_140
696
1 DIVPDNHRNKFKVINVDDDG......NNHQTELEVPRIPRIPTIFG 130 BLOSUM62 Title: Perfect score: Scoring table: Sequence:

0.0 0.7 0.5 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext Total number of hits satisfying chosen parameters:

27513289 segs, 14931090276 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
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-UNFRYT=pto -NORM=ext -HEAPSIZE=560 -MINIEN=0 -MAXLEN=200000000
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-USPR-PROPIED -LARGEQUERY -NGGESCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TINEOUT=120 -WARN TIMEOUT=30 -TRANS-TIMEOUT=30 -TRA

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8: em_estro:*
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em_gss_pro:* em_gss_pln:* em_gss_vrt:* fun: em_estba:* Database :

gp_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	cription	3 Mus m	51075 UI-M-1	1600 Homo	.1602 Mus m	1-M-IU 7667	1785 AL6387	878 AL647878	542	8607 BX848607	10491 AGENCOUR	3389	5693	2662	3369	682	1383	1741	1091	080	7146	119	5347	1691	4334	4794	7562	CDS57174 AGENCOURT	40000	3469	3779	0314	19061	1508 UI-M-EG0	18354 602035	11175 K-EST001	5765 AL845765	57161 EST369	31765 BX331765	20005 603071	45562 NISC_gcl	668 au49d	98956 BX0989	12403 UI-R-E	97442 602395
	ΩH	AK02881	CA75107	AY4116	AY41160	CF74799	78	AL647878	BF61542	BX84860	CF29049	CA79338	BQ7356	BU46266	BJ07336	AL866682	BJ6213	BE68124	AY41160	AL848080	BJ0371	AL859119	CB58534	CB58169	BU70433	BI79479	BX71756	CD557174	CD10959	789874A	BI75779	CB96031	BQ17906	BM95150	BF33835	BM74117	AL845765	AW95716	BX33176	BI5200	CB04556	AI815668	88	BE11240	BG29744
	gth DB	! -	914 1	52	17 2	00	67	21 9	55 1	89 1	79 1	50 1	α	33	1 69	66	27	429 1	27 2	30	67	36 9	87 1	04 1	06	88	86 1	917 14	9.6	1 -	83	37 1	53 1	20 1	97 1	29 1	51 9	23 1	01 1	79	50 1	72 9	74 1	42 1	91 . 16
ď	Query Match	9.86	76	96	93.	92.	00	ω ω	88	88.	88	88	88	88	87.	87.	87.	98	82	83.	80.	78.	78.	78.	75.	74.	73.	73.3	2.5	. 6	70.	69	. 69	. 69	. 69	68.	68.	68.	68	67.	. 99	. 99	65.	65	64
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ALIGNMENTS

AK028913

2918 bp mRNA linear HTC 18-SEP-2003
Mus musculus 10 days neonate skin cDNA, RIKEM full-length enriched
library, clone:4732458E18 product:SUCI-ASSOCIATED NEUROTROPHIC
FACTOR TARGET (FGFR SIGNALLING ADAPTOR) homolog [Homo sapiens],
full insert sequence. AK028813.1 GI:26324755 AK028813.1 GI:26324755 HTTC, CAP trapper. Mus musculus (house mouse) Mus musculus Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, RESULT 1 AK028813 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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/db_xref="FANTOM_DB:4732458E18"
/db_xref="MGI:2390817"
/db_xref="taxon:10090"
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685.00
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                                                                                                                                                                                                                                                                                             genes
                                                                                                                                                                                                                                                                                                                                                                                                                    Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Korno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Yaliwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. Sequencing pipeline with 384 multicapilary sequencer analysis (RISA) system-384 format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation Of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2918)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKBN. Division of Experimental Animal Research in Riken contributed to
  Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                            Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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Please visit our web site for further details.
                                                    Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/tissue_type="skin"
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dev stage="10 days neonate"
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LILYTRKRDSVKWHYLCLRRYGYDSNLFSFESGRRCQTGQGIFAFKCARAEELFNMLQ
EIMQNNSINVVEEPVVERSSHQTELEVPRTPRTPTTPGLGAQNLPNGYPRYPSFGDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHPŠSRHPSVGSARLPSVGEBŠTHPLLVABEQVHTYVŇTTGVQERKNRASVHVPPEA
RVSNAESNIPKEEPSNPEDRDPQVLLKPEGVRFVLGPTPVQKQLMEKEKLEQLGKDPV
SGSGAGNTEWDTGYDSDERRDVPPVNKLVYENINGLSIPSASGVRRGRLTSTSTSDTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NINNSAQRRPALLNYENLPSLPPVWEARKLSRDEDDNLGPKTPSLNGYHNNLDPMHNY
VNTENVTVPASAHKIDYSKRRDCTPTVFNFDIRRPSLEHRQLNYIQVDLEGGSDSDNP
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                                                                                                              372. 1898
/note="unnamed protein product; SUC1-ASSOCIATED NEUROTROPHIC FACTOR TARGET (FGFR SIGNALLING ADAPTOR) homolog [Homo sapiens] (SPTR AAH21562, evidence: FASTY, 95.5%ID, 100%length, match=1536)
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AY411600
Homo sapiens HCM4278 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
AY411600
AY411600.1 GI:39767568
                                                                                                                                                                  101 AsnValValGluGluProValValGluArgAsnAsnHisGlnThrGluLeuGluValPro 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clark, A.G. (Janowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G. (Janowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Mang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-Nov-2003) Celera Genomics, 45 West Gude Drive, Snokokille, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
503 CTGTTTTCTTTTGAAAGTGGTCGAAGGTGTCAGACTGGACAAGGAATTTTTGCTTTTAAG
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                                                                                          91 AATGAGTTAGGTTCTGGCATAATGGAACTTACAGACACAGAACTGATTTTATACACCGGC
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Science 302 (5652), 1960-1963 (2003)
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/db_xref="taxon:9606"
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National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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AAACGTGACTCAGTAAAATGGCACTACCTCTGCCTGCGACGCTATGGCTATGACTCGAAT
                                                                         CICITITICITITICAAAGIGGICGAAGGIGICAAACIGGACAAGAAAICITITICCITITAAG
                                               LeuPheSerPheGluSerGlyÅrgArgArgCysGlnThrGlyGlnGly1lePheAlaPheLys
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/strain=".orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb./pu/orb.
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CF747997.1 GI:37644341
EST.
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Tissue Procurement: Dr. James Lin Unive
CDA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
210
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Mus musculus
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Musinae; Musinae
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Location/Qualifiers
1. 800
/ coganism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
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Score:

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FEATURES
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with EcoR I adaptor , digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TTATTGAAGT. This library was created for the University lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
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Sanger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: LIE8b02.sp6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
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. (bases 1 to 567)
Huckle,E., Taylor,R., Ashurst,J.L., Zorn,A.M. and Rogers,J.
Sanger Xenopus tropicalis EST project 2001 (10_2001)
Unpublished (2001)
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                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
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AL638785 XGC-egg Silurana
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AL638785.1 GI:16790764
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97.67%
95.35%
91.95%
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Sanger Institute
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Best Local Similarity:
Query Match:
DB:
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AL638785
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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No.:
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AUTHORS
TITLE
JOURNAL
COMMENT
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mRNA linear EST 20-NOV-2003 tropicalis cDNA clone TGas039c07 5',
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Silurana tropicalis
Silurana tropicalis
Bukaryota; Metazca; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana
1 (bases 1 to 721)
Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)
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/lab_host="Escherichia coli XLI-blue"
/clone lib="XGC-egg"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cD
was oligo dT primed from Sug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 AsnGluLeuGlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArg
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Contact: Huckle E
Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-757-415A-1_COPY_11_140 (1-130) x AL638785 (1-567)
Location/Qualifiers
1. 567
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/mol_type="mRNA"
/db xref="taxon:8364"
/clone="LIE8b02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
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EST.
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Percent Similarity:
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Query Match:
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/ Organism="Xenopus laevis"

/ Mol_type="mRNA"

/ Mol_type="mRNA"

/ Ab_tef="taxon:8355"

/ Clone="IMAGE:374439"

/ Lissue_type="gastrula (stages 10.5, 11.5 mixed)"

/ Lissue_type="gastrula (stages 10.5, 11.5 mixed)"

/ Lissue_type="gastrula forms 10.5, 11.5 mixed]

/ Rocal The library was mass excised and xelous at the 3'

end The library was mass excised and used to infect

ToploF'. Clones were picked into freezing medium (per

Ilter 15 g tryptone, 10g yeast extract, 5g NaCl, 36 mM

KZHPO4, 13.2 mM KHZPO4, 1.7 mM Na-citrate, 0.4 mM MgSO4 7

HZO, 6.8 mM (NH4) ZSO4, 4 % w/v glycerol) and grown for 24

hours. Orliana library construction by Bruce Blumberg

(Cho et al 1991 Cell 67, 1111-1120)."
                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manbhibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopos.

1 (bases 1 to 55)
1 (bases 1 to 55)
2 (bases 1 to 55)
2 (bases 1 to 55)
3 (bases 1 to 55)
4 (bases 1 to 55)
5 (bases 1 to 55)
6 (bases 1 to 55)
7 (bases 1 to 55)
8 (bases 1 to 5)
8 (bases 1 to 5)
8 (bases 1 to 5)
8 (bases 2 to 5)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu.
Library constructed by Bruce Blumberg
Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing
Source lab clone id - xlnnga006hle This clone is available
royalty-free through LiMi, contact the IMAGE Consortium
(image@image.llnl.gov) for further information.
Seq primer: -40RP from Gibco
High quality sequence stop: 419.
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Mismatches:
Indels:
                                                                        Xenopus laevis (African clawed frog)
Xenopus laevis
   BF615429.1 GI:11789019
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                         Email: trop@sanger.ac.uk
This sequence is from a Xenopus Gene Collection (XGC) library
CDNS tructed by Aaron M. Zon.
CDNA was oligo dT primed from 5ug of poly A+ RNA from stages 10-13
gastrulae. ECORI-NotI cut CDNA was then ligated into pCS107 with
CocNI at the 5' end and NotI at the 3' end.
Vector: pCS107; Site 1: ECORI; Site 2: NotI
Host: Escherichia coli XLI-blue
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_ESQUENCE_ID: TGas039c07.plkSP6
Sequencing primer: SF6
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="gastrula (stages 10.5-12 mixed)"
/lab host="Escherichia coli XL1-blue"
/clome_lib="XGC-scherichia coli XL1-blue"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA was oligo dT primed from 5ug of poly A+ RNA from stages into 10-13 gastrulae. EcoRI.NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end.".
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Silurana tropicalis"
/mol_type="mRNA"
/do_xref="taxon:8364"
/clone="Toas039007"
   CB10 1SA, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ArgThrProArgThrProThrThrProGly 130
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Hinxton, Cambridgeshire,
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Query Match: 88.58% Indels: 1 DB: 13 Gaps: 1 US-09-757-415A-1_COPY_11_140 (1-130) x BX848607 (1-689) Qy 1 ASPTHYVALPYCASPASHHISAYGASHLYSPHELYSVALILEASPASPASPGIY 20 1:::	0y 41 LysArgAspSerValLysTrpHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsn 60 324 AAGAGAGTTCTGTCAAGTGGCCTTACCTTGCGACGCTATGGATACGATTCAAAC 383 Qy 61 LeuPheSerPheGluSerGlyArgArgCygGlnThrGlyGlnGlyIlePheAlaPheLys 80	Qy 101 AsnValValGluGluProValValGluArgAsnAsnHisGlnThrGluLeuGluValPro 120 Db 504 AGTGTTGTAGAGGAGCCTGTAGTTGAACGAAATCCCCAGACCCAGTTGGATGTTCCA 560 Qy 121 ArgThrProArgThrProThrThrProGly 130 Db 561 AGAACCCTCGCACACCCATACCCTGGC 590 RESULT 10 779 bp RESULT 10 779 bp CF290491 779 bp DEFINITION AGENCOURT 15201759 NICHD XGC_Emb4 Xenopus laevis cDNA clone ACCESSION CF290491 779 bp VERSION CF290491 779 bp RESULT 10 779 bp ACCESSION CF290491 779 bp RESULT 10 779 bp ACCESSION CF290491 779 bp RESULT 10 779 bp	NISM NCE ORS B NAL	found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bpry/image/image.html Plate: LiAMA12174 row: 1 column: 17 High quality sequence stop: 665. FEATURES Location/Qualifiers ource 1. 779 / organism="Xenopus laevis" / forganism="Xenopus laevis" / db xref="taxon: RRNA" / lab_host="thiob" (phage-resistant)"
Oy 61 LeupheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePheAlaPheLys 80 226 CTTTTTCTTTTGAAGTGGACGAAGGTCAAGAATATTTGCTTTTAAA 285 Oy 81 CysAlaArgAaGluGlubeuPheAshMetLeuGlaGlaGlaGAshAshSerIle 100	OY 121 ArgThrProArgThrProGly 130 Db 403 AGAACCCTCGCACACCACCCCTGGA 432 RESULT 9 RA48607 LCCUS BX848607 BX848607	clawed frog) rdata; Craniata; Vertebrata; Butel ura; Mesobatrachia; Pipoidea; Pipi ters,M., Radelof,U., Schneider,D., Landgrebe,J. Set 1 (RZPDLIB No.988) enzentrum fuer Genomforschung GmbH , D-69120 Heidelberg, Germany A Clone Collection (amp-resistant	Dany products Snowlib pp. 1-37 responser 110 No.298 Arabusis and public policy of the policy for for the policy for further information. Seq primer: FEATURES 1. 689	/note="Organ: whole embryo; Vector: pcMV-SPORT6; Site_1: Note: State_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size_2: Lkb. Constructed by Life Technologies. Note: This is a Xenopus Gene Collection (XGC) library." Alignment Scores: 1.23e-68 Length: 689 Score: 616.50 Matches: 117 Percent Similarity: 95.38* Conservative: 7 Best Local Similarity: 90.00\$ Mismatches: 5

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/clone lib="NICHD XGC Emb4"
/note="Organ: whole embryo; Vector: pCMV.SPORT6; Site 1:
NotI; Site 2: SalI; Cloned unidirectionally. Primer: Öligo
dI. Average insert size 2.1 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) library."
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AGENCOURT 10256250 NICHD XGC Emb1 Xenopus laevis cDNA clone
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(Apases 1 to 850)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                       AsnGluLeuGlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArg
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: Capbbs-remail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information (found through the I.M.A.G.E. Consortium/LLNL) at:
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AGENCOURT 8149157 NICHD XGC Emb4 Xenopus laevis cDNA clone
IMAGE:5570479 5', mRNA sequence.
BQ735693.
BQ735693.1 GI:21874590
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1 (bases; Lo 885)

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Xenopus laevis
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Plate: LLAMiliss ...
High quality sequence stop: 6
Location/Qualifiers
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616.50
95.38%
90.00%
88.58%
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/lab_host="adult"
/lab_host="adult"
/lab_host="adult"
/clool_lib="CSEQRRN19"
/note="0rgan: ovary; Vector: pBluescript II KS(+); Site_1:
Constructed from 1 million independent clones. cDnA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to Not! adapters, digested with
EcoRI, size-selected, and cloned into the Not! and ECORI
compartible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9212 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 733)
Boardman, P. B., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken CDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 GluLeuThrAspThrGluLeuIleLeuTyrThrArgLysArgAspSerValLysTrpHis
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                                                                                                                                                                                                                                                                       Department of Biomolecular Sciences University of Manchester Institute of Science and Technology (UMIST)
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Mismatches:
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/mol_type="mRNA"
/strain="Layer"
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                                                                                                                                                                                                                                                                                                                                      PO Box 88, Manchester, M60 1QD, UK
                                                                                                                                                                                                                                                                                                                                                                                                   Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1. .733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9031"
/clone="ChEST271g4"
Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'sex="Female"
                                                                                                                                                                                                                                                     Contact: Simon Hubbard
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98.36%
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88.07%
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Fax: 01612360409
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                             /dev stage="embryo, stage 31-32"
/lab host="DH10B (phage-resistant)"
/lone_lib="NICHD XGC Embh"
/note="Organ: whole embryo; Vector: pCMV-SPORT6; Site_1:
Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Ōligo
Tr. Average insert size 2.1 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) library."
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603368412F1 CSEQRBN19 Gallus gallus cDNA clone ChEST271g4 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 AATGAGCTTGGCTCTGGCATAATGGAATTGAGAAAAATGAACTCATCTTATACACTCGC 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LysArgAspSerValLysTrpHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsn 60
                                                            CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: 'Agencourt Bioscience Corporation
Clone distribution: NGT-CGAP clone distribution information can l
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Plate: LiAM12312 row: m column: 08
High quality sequence stop: 550.
Location/Qualifiers
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Matches:
                                                                                                                                                                                                                                                                            /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:5570479"
  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Igor Dawid
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Silurana tropicalis (western clawed frog)
Silurana tropicalis
Silurana tropicalis
Silurana tropicalis
Silurana tropicalis
Enkaryota, Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia) Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.

CE Croning, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.
Sanger Xenopus tropicalis EST project 2001 (11_2003)
AL Unpublished (2003)
On Sep 15, 2002 this sequence version replaced gi:22886947.
Contact: Taylor R
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: tropesanger.ac.uk
Sanger Institute
Hinxton, Cambridgeshire, CB10 Teggl26g01.plkaSP6
Sequencing Primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
Constructed by Aaron M. Zorn.
CONSTRUCTED ALL BECONT AT THE SCORI AT THE SCORI-NOTI AT THE 3' end.
Vector: PCS107; Site 1: ECCATION WILL-blue.

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers
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/mol type="mRNA"
/db Zref="Laxon:834"
/db Zref="Laxon:834"
/db Zref="Experience on the propies of the propies
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                                                                   464 CTITITICITITGAAAGTGGACGAAGGAGGTGTCAGACTGGACAAGAATAITTGCTITITAAA 523
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Conservative:
Mismatches:
Indels:
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                                                                                                                                243 AATATGTTGCAAGAGATAATGCAGAATAATAGTATAATGTGGTAGAAGAACCAGTAGTA 302
89 AsnMetLeuGlnGluIleMetGlnAsnAsnSerIleAsnValValGluGluProValVal 108
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Unpublished (2001)
Conteact: Tada (2001)
Conteact: Resource Information
National Institute of Genetics.
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6856
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and
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| db xref="texon:815s"
|clon="X1109m21"
| tissue_type="whole embryo"
| dev stage="stage 25"
|clone_lib="NIBB Mochii normalized Xenopus tailbud
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Matches:
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Location/Qualifiers
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/organism="Xenopus laevis"
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DB:
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KEYWORDS
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AUTHORS
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285 AATGAGCTTGGCTCTGGCATAATGGAATTGACAGAAATGAGTGAATCTTATACACTCGT 344
                                                                                              345 AAGCGAGATTCTGTCAAGTGGCCTTACCTCTGCTTGCGACGCTATGGATACGATTCAAAC 404
                                                                                                                                      101 AsnValValGluGluProValValGluArgAsnAsnHisGln-ThrGluLeuGluValPr 120
                                                                                                                                                                                                                     21 AsnGluLeuGlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArg 40
                                                                               41 LysArgAspSerValLysTrpHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsn 60
                                                                                                                         61 LeuPheSerPheGluSerGlyArgArgArgCysGlnThrGlyGlnGlyllePheAlaPheLys 80
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Sequence 49, Appl Sequence 1644, Ap Sequence 157, App Sequence 89, Appl Sequence 5, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli

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RESULT 1

US-08-787-091-1

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US-08-787-091-1

Sequence 2, Sequence 2, Sequence 2, Sequence 2, Sequence 1, Application US/08787091

Patent No. 6100366

GENERAL INFORMATION:

APPLICANT: Carpino, Nicholas A. APPLICANT: Wisniewski, David G. APPLICANT: Wisniewski, David G. APPLICANT: Strift, Annabel O'C. APPLICANT: Strift, Annabel O'C. APPLICANT: Strift, Annabel O'C. APPLICANT: Clarkson, Bayard D. TITLE OF INVENTION: Chronic Myelogenous Leukemia 1TITLE OF INVENTION: Chronic Myelogenous Leukemia NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington COUNTRY: US

ZIP. 2
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ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMENT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/787,091
                                  4 US-09-891-641-49
4 US-09-134-641-49
4 US-09-134-641-49
4 US-09-134-838-89
4 US-09-130-891-57
4 US-09-130-891-5
3 US-09-130-840-1
3 US-09-130-840-1
3 US-09-130-810-5
4 US-09-130-811-24
4 US-09-456-1
5 US-09-134-001C-1594
5 US-09-134-001C-1594
6 US-09-623-624-1
7 US-09-134-001C-1058
7 US-09-215-694-18
7 US-09-134-001C-1058
7 US-09-136-421B-1
7 US-09-134-001C-1058
7 US-09-136-421B-1
7 US-09-136-001-2650
7 US-08-91-27-170
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REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL96-05PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIPICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,418
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
Sequence 854, App
Sequence 855, App
Sequence 842, App
Sequence 91, Appl
Sequence 12526, A
Sequence 1386, Appli
Sequence 1, Appli
Sequence 1, Appli
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16, Appl
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Appli
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                                                                                           August 8, 2004, 21:10:45; Search time 99.2105 Seconds (without alignments) 727.177 Million cell updates/sec
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1 DTVPDNHRNKFKVINVDDDG......NNHQTELEVPRTPRTPTFG 130
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2: 'cgn2 6/ptodata/2/ina/5B COMB.seg:*
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6: 'cgn2 6/ptodata/2/ina/PCTUS COMB.seg:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                     - nucleic search, using frame_plus_p2n model
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US-09-453-702B-91
US-09-621-976-12526
US-09-023-655-1386
US-08-685-1386
US-08-896-164-44
US-08-891-443BB-3
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Maximum Match 100%
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Database :

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Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 15352450 Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 10, Appli Sequence 105, Appl Sequence 105, Appli Sequence 1058, Appli Sequence 1056, Appli Sequence 1076, Appli

Sequence 1 Sequence 2 Sequence 2

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Wang, Zhiwei
John Tillinghast
  FILE REFERENCE: 784CIP2B
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                                                                                                                                                                                   SEQ ID NO 854 LENGTH: 1146
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APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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Sequence 854, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
                 TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1446 base pairs TYPE: nucleic acid STRANDEDNESS: single
TELECOMMUNICATION INFORMATION
                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                            3.13e-10
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47.32%
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APPLICANT: Tang, Y. Tom
APPLICANT: Asundi, vinod
APPLICANT: Cheng, Jie
APPLICANT: Chen, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Wehrman, Tom
APPLICANT: Wen, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Ang, Jian-Rui
APPLICANT: Zhou, Ping
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John Tillinghast
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Wang, Dunrui
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81 CysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGluIleMetGlnAsnAsnSerile 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        825 AAGGTCAAACTGGTGATGTGGCCTCTCAGCTCACTGAGGAGATACGGTCGGGACTCAACG 684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PL_Penes Version 1.0
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GENERAL INFORMATION:
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
norticant: Zhang, Jie
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Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
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Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
; LOCATION: (109)...(1122)
US-09-620-312D-854
                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ma, Yunqing
Wang, Dunrui
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Best Local Similarity:
Query Match:
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Percent Similarity:
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NAME/KEY: CDS
LOCATION: (334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 CysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGluIleMetGlnAsnAsnSerIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 ACAAGGGAAGGAGAA-----ATGATCTATCAGAAGGTTCATTCTGCGACACTG 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 AsnvalvalgluGluProValValGluArgAsnAsnHisGlnThrGluLeuGluValPro 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---CATGAAAGATTAATGCTAGAAATGGAA 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 Servaliys------TrpHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsn 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LeuPheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePheAlaPheLys 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 GlySerGly1leMetGluLeuThrAspThrGluLeuIleLeuTyrThrArgLysArgAsp 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-757-415A-1_COPY_11_140 (1-130) x US-09-620-312D-855 (1-914)
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 65666621 Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REPERENCE: 784CIP28
CURRENT PRESENCE: 784CIP28
CURRENT PILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR PILING DATE: 2000-07-19
PRIOR PILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOPTWARE: PL_Genes Version 1.0
SEQ ID NO 855
                                                                                                                                                                                                                                                                                                                                                               914
203
113
3
                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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835 CAGAAGGCCCGGGTAAGGCCCCTTCCT 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 842, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
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133.50
48.62%
30.28%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Chen, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
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Wang, Jian-Rui
Zhou, Ping
Ma, Yunging
                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                , NAME/KEY: CDS
; LOCATION: (109) .. (867)
US-09-620-312D-855
                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-620-312D-842
                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                   FEATURE
                                                                                                                                                                                                                                                                                                                                                                     No.:
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.042 GICCIGCIGGAAAIGGAGAAGAACGIGAGGCIGCIGAACAAGGGCACGGAACAITACICG 1101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            862 GICTCGTGGCCCTCTGCTCACTGCGCCGCTATGGCCGGGATGCCACGCTTTACCTTC 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlusergiyArgArgCysGlnThrGlyGlnGlyIlePheAlaPheLysCysAlaArgAla 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 -----TrpHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsnLeuPheSerPhe 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------GlnAsnAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 MetGluLeuThrAspThrGluLeuIleLeuTyrThrArgLysArgAspSerValLys---
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TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-757-415A-1_COPY_11_140 (1-130) x US-09-620-312D-842 (1-2735)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2735
31
19
48
APPLICANT: Wang, Zhiwei
APPLICANT: Onn Tillinghaet
APPLICANT: John Tillinghaet
APPLICANT: John Tillinghaet
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 656662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: POLYPEPE
CURRENT APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
NUMBER OF FOLING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SEQ ID NO 842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
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Matches:
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STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
US-09-453-702B-91/C
; Sequence 91, Application US/09453702B
; Patent No. 6565723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
Burland, ... on Palexie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1102 TATCCCTGCACACCCACGACC 1122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burland, Valer
Perna, Nicole T.
Plunkett, Guy
Welch, Rod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               776-07
124.50
46.73%
28.97%
17.89%
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (334)..(1314)
US-09-620-312D-842
                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity:
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1210 cecceaectriarenterearinareaccecaaceeaaceaacaaaceirceaetric
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1090 CAGGIAATATTAAAGATGCGACAATTGTTTATAAGGCAAAGAAGAAGTATAAAATTTCACTTC 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .150 CAGGAGTGGAACATTTATCGCAGGTTATGGATATTGCTGAACTTATAGAȚAACCAAAATG 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1030 ATTTÖTTTGGTGGTTTTTAAGTTTTAAAACCATGCGAGTTATTGACAATGAAT 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::: |||||| :::|||
----TCGAATGCAGGCAATATTTTACGAGAAT 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 ArgAsnLysPheLysValIleAsnValAspAspAspGlyAsnGluLeuGlySerGlyIle 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----LysArgAspSerValLysTrpHisTyr 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .------LeuThrAspThr 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 ThrGlyGlnGlyIlePheAlaPheLysCysAlaArgAlaGluGluLeuPheAsnMetLeu 91
COMPTRY TA

COUNTRY TA

ZIP: 53701-2113

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: Diskette, 3.50 inch. 1.44Mb storage

COMPUTER: Diskette, 3.50 inch. 1.44Mb storage

COMPUTER: Diskette, 8.00

SOFTWARE: Word Prefect 8.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/453,702B

FILING DATE: 04-DEC-1999

PRIOR APPLICATION NUMBER: 60/110,955

PILING DATE: 04-DEC-1998

ATTORNEY/AGENT INFORMATION:

NAME: Seay, NICADLAS J.

REGISTRATION NUMBER: 27386

REFERENCE/DOCKET NUMBER: 27386

REFERENCE/DOCKET NUMBER: 960296.95017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-757-415A-1_COPY_11_140 (1-130) x US-09-453-702B-91 (1-1813)
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 91:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 91
SEQUENCE CHARACTERISTICS
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83.00
40.98%
24.59%
11.93%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
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RESULT 6 . US-09-621-976-12526

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328 AAGGICAAACIGGIGAIGIGGCCICTCAGCICACIGAGGAGAIACGGICGGGACICAACG 387
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US-09-023-655-1386
Sequence 1386, Application US/09023655
Patent No. 6607379
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Office of Sequence
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESSED: INVENTE BHARMACHUICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-757-415A-1_COPY_11_140 (1-130) x US-09-621-976-12526 (1-415)
                              GENERAL INCORPATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Johnert, S.
APPLICANT: Glordano, J.Y.
ITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENERT, 0.54 PR.
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 12526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/023 FEF
CLASSTEATS: HERFUTT.
                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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Sequence 12526, Application US/09621976
Patent No. 6639063
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
                                                                                                                                                                                                                                                                                                                                                                                                                       82.50
52.08%
41.67%
11.85%
                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                   US-09-621-976-12526
                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                         LENGTH: 415
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1738 -----GTGGATGACTCTGTGGTGGCCCAGAAC 1764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 GlnGluIleMetGlnAsnAsnSerIleAsnValValGluGluProValValGluArgAsn 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 ThrGlyGlnGlyIlePheAlaPheLysCysAlaArgAlaGluGluLeuPheAsnMetLeu 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 LeuArgArgTyrGlyTyrAspSerAsnLeuPheSerPheGluSerGlyArgArgCysGln 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: No. 58277300 No. 5827730disk of No. 5827730th America STREET: 405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-757-415A-1_COPY_11_140 (1-130) x US-09-023-655-1386 (1-5828)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08557139
Patent No. 582730
GENERAL INFORMATION:
APPLICANT: Pedersen, Oluf
APPLICANT: Bjorbak, Christian
APPLICANT: Bjorbak, Christian
APPLICANT: Prederiksen, Kathrine A.
TITLE OF INVENTION: MUTANT DNA ENCODING INSULIN RECEPTOR
TITLE OF INVENTION: SUBSTRATE 1
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BEAP C compatible
SOFWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1711 ACGGGCCCGGGGAGTTCTGGATGCAG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 AsnHisGlnThrGluLeuGluValProArg 121
RECISTRATION NUMBER: 37,071
REPERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
ITELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1386:
SEQUENCE CHARACTERISTICS:
LENGTH: 5828 base pairs
ITYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels:
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NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4041.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/557,139
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FILING DATE: 12-FEB-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                            78.00
40.00%
30.00%
11.21%
                                                                                                                                                                                                                                          TOPOLOGY: linear
| IMMEDIATE SOURCE:
| LIBRARY: GENBANK
| CLONE: 9386256
US-09-023-655-1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
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US-08-557-139-1
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1214 ATCAGGCGCTGTGGCCACTCGGAAAACTTCTTCTTCATCGAGGTGGGCCGTTCTGCCGTG 1273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 LeuargargTyrGlyTyrAspSerasnLeuPheSerPheGluSerGlyArgArgCysGln 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 ThrGlyGlnGlyIlePheAlaPheLysCysAlaArgAlaGluGluLeuPheAsnMetLeu 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CBATA, Yuichi
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ASSOCIATED
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ASSOCIATED
TITLE OF INVENTION: WITH GASTRIC CANCER AND METHODS FOR
TITLE OF INVENTION: B7
NUMBER OF SEQUENCES: B7
ADDRESSEE: Felfe & Lynch
STREET: B05 Third Avenue
CITY: New York City
STATE: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-757-415A-1_COPY_11_140 (1-130) x US-08-557-139-1 (1-6152)
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REGISTRATION NUMBER: 30,946
REFERENCE/DOCKST NUMBER: LUD 5499 - JEL/NDH/SLH
TELECONUNINATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches:
Indels:
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MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb
COMPUTER: IBM PS/2
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OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDERfect
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/08/896,164
FILING DATE: UJ/y 17, 1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 44, Application US/08896164; Patent No. 6218521; GENERAL INFORMATION:
                   TELEPHONE: (212) 867-0123
TELEPAX: (212) 878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6152 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                        DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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78.00
40.00%
30.00%
11.21%
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581..4309
                                                                                                                                                                                    linear
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                     NAME/KEY:
LOCATION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---CCCTATGACTGTNNTCACTGTGGGAAAAGCTTCAATCATNAAACAAACCTCAATAAA 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   555 CATGAGCGAÁTÍCNTACAGGAGÁGAAACCÍTATTCCTGTTCTCAGTGGGAAAAAACTTC 614
                                                                                                                                                                                                                                                                                                                                                                       22 GluLeuGlySerGlyIleMetGluLeuThr-----AspThrGluLeuIleLeuTyr 38
                                                                                                                                                                                                                                                                                                                                                                                                                                       39 ThrargLysArgAspSerValLysTrpHisTyr----LeuCysLeuArgArgTyrGly 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 TyrkspSerAsnLeuPheSerPheGluSerGlyArgArgCysGlnThrClyGlnGlylle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 PheAlaPheLysCysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGluIleMetGln
                                                                                                                                                                                                                                                                           US-09-757-415A-1_COPY_11_140 (1-130) x US-08-896-164-44 (1-698)
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Sequence 3, Application US/08531439B

Patent No. 598702

GENERAL INFORMATION:
APPLICANT: Beach, David

ITILE OF INVENTION: Cyclin/CDK Associated Proteins,
ITILE OF INVENTION: Cyclin/CDK Associated Proteins,
ITILE OF INVENTION: and Uses Related Thereto

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:
ADDRESSES: Foley, Hoag & Eliot

STREET: One Post Office Square

CITY: Boston

STATE: WA

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 AsnAsnSerIleAsnValValGluGluProVal------
                                                                                                                                                                  698
227
230
50
623
                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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N: 435
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MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION NUMBER: US/08/531,4391
FILING DATE: 21-SEP-1995
CLASSIFICATION: 435
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 44
SEQUENCE CHARACTERISTICS:
LENGTH: 698 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                0.203
77.50
43.85%
20.77%
                                                                                                 linear
                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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                                                                                                                                             Alignment Scores:
                                                                                                 TOPOLOGY:
                                                                                                                US-08-896-164-44
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DB:
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556 AAGAGGTGGTATCGCCTAGCGTCTGATGAGTCTCTATGGCAGACCTTAGACCTTACA--- 612
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838 GATCCCATTGTCAATACTCTCGCAAAAAACTCAAATTTAGTGCGACTTAACCTTCCTGGG 897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 ProAspAsnHisArgAsnLysPheLysVallleAsnValAspAspAspGlyAsnGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 -----LeuTyrThrArgLysArgAspSerValLysTrpHisTyrLeuCysLeuArgArg
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Matches:
Conservative:
Mismatches:
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ALECTOR VINCENT, MALL...

NAME: VINCENT, MALL...

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: CSV-006.01

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-7000

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1600 base pairs

"WITH INCOME ACID NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 100 NO: 1
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US-09-023-655-1505
; Sequence 1505, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 ThrProArgThrProThrThrPro 129
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75.00
36.90%
23.81%
10.78%
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TOCATION: 148..1452
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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US-08-531-439B-3
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1953 GTGCTCCCCAAGCCAAGCTTCCACCATCACGTTCTGGGTCAACATCTYTAAYTGMAGC 2012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----IleAsnValValGluGluPro 106
                                                                 :::|||:::|||
838 GATCCCATTGTCAATACTCTCGCAAAAACTCAAATTTAGTGCGACTTAACCTTCCTGGG 897
                                        --MetGlnAsnAsnSerIleAsnVal---ValGlu 104
                                                                                                                  GluproValValGlu-----ArgAsnAsnHisGlnThrGluLeuGluValProArg 121
  118 AGCCCTTTTCGTGTACAGGACATGGACCTATCGAACTCAGTTATAGAAGTGTCCACCCTC 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 GlyTyrAspSerAsnLeuPheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGly 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1773 GACCGGGGCCTGCCATCCCTCACCTCTGTGTCCTGGAACATCAGCGTGCCCAGAGACCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 -----IlePheAlaPheLysCysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-757-415A-1_COPY_11_140 (1-130) x US-09-489-847-16 (1-2209)
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rosen et al
TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: PZ031P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/489,847
CURRENT FILING DATE: 2000-01-24
EARLIER APPLICATION NUMBER: PCT/US99/17130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: 60/095,486
EARLIER FILING DATE: 1998-08-05
EARLIER APPLICATION NUMBER: 60/095,319
EARLIER FILING DATE: 1998-08-12
EARLIER APPLICATION NUMBER: 60/095,454
EARLIER FILING DATE: 1998-08-06
EARLIER FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 376
SOFTWARE: PATCHTIN VOIT: 2.0
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                                                                                                                                                                                                  122 ThrProArgThrProThrThrPro 129
                                                                                                                                                                                                                                       398 IGICCIGGALTCCCTAAATTICCC 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
EARLIER PEDLICATION NUMBER: 60/095,486
EARLIER FILING DATE: 1998-08-05
                                                                                                                                                                                                                                                                                                             Sequence 16, Application US/09489847
Patent No. 6476195
GENERAL INFORMATION:
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39.50%
25.21%
10.70%
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ORGANISM: Homo sapiens
US-09-489-847-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
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LENGTH: 2209
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProAspAsnHisArgAsnLysPheLysValIleAsnValAspAspAspGlyAsnGluLeu
COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE EXPRESSION 1508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---GluGluLeuPheAsnMetLeuGlnGluIle--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-757-415A-1_COPY_11_140 (1-130) x US-09-023-655-1505 (1-1600)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 GlySerGlyIleMetGlu---LeuThrAspThrGluLeuIle----
                                                                                                                                                                                ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PEFECT 6.1 for Windows/MS-DOS
CURRATI APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                     HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (650) 845-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 150
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1600 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.00
36.90%
23.81%
10.78%
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: sing
            IITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                          PALO ALTO
CALIFORNIA
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Best Local Similarity:
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US-09-023-655-1505
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                                                                                                                                                                   COUNTRY:
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                                                                                                                          CITY: 1
STATE:
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DB:
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                                                                                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (309398)...(309398)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (309418)...(309418)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
LOCATION: (31287)...(312837)
OTHER INFORMATION: nequals a, t,
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (312993)...(312993)
OTHER INPORMATION: n equals a, t,
NAME/KEY: misc_feature
'LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (559167)..(559167)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals a,
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LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a,
                                                                                     NAME/KEY: misc feature
LOCATION: (234220) ..(234220)
OTHER INFORMATION: n equals a,
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LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a,
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LOCATION: (674435)
OTHER INFORMATION: n equals a,
NAMENCEY: misc feature
LOCATION: (682442)...(682442)
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LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a,
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LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a,
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LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a,
                                         LOCATION: (234187) .. (234187)

STHER INFORMATION: n equals a,
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LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
n equals a,
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INFORMATION: n equals a,
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INFORMATION: n equals a,
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INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
                     NAME/KEY: misc_feature
LOCATION: (234187)..(2
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APPLICANT: Bull et al.

APPLICANT: Bull et al.

APPLICANT: Bull et al.

Patent No. 6503729

TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ TITLE OF INVENTION: jannaschii
FILE REPERRNCE: P8275

CURRENT APPLICATION NUMBER: US/08/916,421B

CURRENT FILING DATE: 1997-08-22

PRIOR PILING DATE: 1996-08-22
                                                            2013 CCCACGAGCGGCAAGCAGCTAGACCTGCTCTCCGGTGACACTTACCCCAAGGACT 2069
                 107 ValValGluArgAsnAsnHisGlnThrGluLeuGluValProArgThrProArgThr 125
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LOCATION: (98343)...(98143)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature

LOCATION: (103998)...(103998)

OTHER INFORMATION: n equals a, t, c, or g

LOCATION: (148948)...(148948)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature

LOCATION: (163385)...(163385)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature

LOCATION: (191989)...(191989)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature

LOCATION: (191989)...(191995)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature

LOCATION: (191995)...(191995)

OTHER INFORMATION: n equals a, t, c, or g

NAME/KEY: misc_feature

LOCATION: (191995)...(191995)
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                                                                                                                                                    Sequence 1, Application US/08916421B Patent No. 6503729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (98159)..(98159)
OTHER INPORMATION: n equals a, t,
LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
NOCATION: (28222)..(28222)
OTHER INPORMATION: n equals a, t,
NAME/KEY: misc_feature
...httoN: (28257)..(28258)
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OTHER INFORMATION: n equals a, t,
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LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a,
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LOCATION: (98256). (98266)
OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
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LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a,
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INFORMATION: n equals a,
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SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 1664976
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                                                                                                                                                                                                                                    FEATURE:
COTHER INFORMATION: CDC 1551
COTHER INFORMATION: "n" bases at various positions throughout the sequence
CTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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APPLICANT: FASER, Claire M.
APPLICANT: FASER, Claire M.
APPLICANT: FASER, Claire M.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBRICULOSIS
FILE REFERENCE: 24366-220007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFFWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
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TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM_

TITLE OF INVENTION: TUBERCULOSIS
FILE REPERENCE: 24366-220007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LIENGTH: 14103765
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Mismatches:
Indels:
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Matches:
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Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, ROBERT
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27.27%
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US-09-103-840A-1/c
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Matches:
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Patent No. 629428
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, JOHN C.
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LOCATION: (1313224).
UCATION: (1313224).
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NAME/KEY: misc_feature
LOCATION: (1349473).
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COTHER INFORMATION: n equals a, t
NAME/ANI (113081). (113081)
COTHER INFORMATION: n equals a, t
OTHER INFORMATION: n equals a, t
NAME/ANI (131098). (131098)
LOCATION: (131098). (131098)
OTHER INFORMATION: n equals a, t
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OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
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LOCATION: (1664854)..(1664855)
OTHER INFORMATION: n equals a,
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DTHER INFORMATION: n equals a, NAME/KEY: misc_feature
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THER INFORMATION: n equals a,
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Best Local Similarity:
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US-09-103-840A-2/c
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2085929 GTCGACACTGACGCCAGCGAGGTTCGAAGGCATCATGGATGCCCTATTCACCGGCCTG 2085870
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                                                                                                                         4411529
33
22
49
17
                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
; TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                       2.44e+05
74.00
45.45%
27.27%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Search completed: August 9, 2004, 00:57:52 Job time : 2545.21 secs

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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

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US-09-436-116-5
US-09-436-116-3
US-10-34-887-1165
US-10-172-118-1165
US-10-334-143-155
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US-10-146473.

Publication No. US200301088881

GENERAL INFORMATION:

APPLICANT: Scanlan, Matthew

APPLICANT: Gout, Ivan

APPLICANT: Gout, Ivan

APPLICANT: Grockert, Elisabeth

APPLICANT: Grockert, Elisabeth

APPLICANT: Grockert, Stockert, Stockert,

APPLICANT: Glat, Nao-Tseng

APPLICANT: Chen, Yao-Tseng

APPLICANT: Chen, Wao-Tseng

APPLICANT: Chen, Woods

ILE COF INVENTION: Breat Cancer Antigens

FILE COF INVENTION: Breat

FILE COF INVENTION: Breat

FILE REFERENCE: LO0461/7013 (JRV)

CURRENT FILING DATE: 2002-05-15

PRIOR PILING DATE: 2002-05-15

NUMBER: PAPPLICATION NUMBER: US 60/291,150

PRIOR FILING DATE: 2001-05-15

NUMBER: PatentIn Version 3.0

SEQ ID NO 27

TYPE: DNA

CRGANISM: Homo sapiens
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-FGAPOP=6 - FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5
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1 DTVPDNHRNKFKVINVDDDG.....NNHQTELEVPRTPRTPTTPG 130
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1. \cgn2_6/ptodata/1/\tilde{\text{Dubpna/USO7}} \text{PUBCOMB.seq:*}

2. \cgn2_6/ptodata/1/\tilde{\text{Dubpna/USO7}} \text{NEW PUB.seq:*}

3. \cgn2_6/ptodata/1/\tilde{\text{Pubpna/USO6}} \text{NEW PUB.seq:*}

4. \cgn2_6/ptodata/1/\tilde{\text{Pubpna/USO6}} \text{NEW PUB.seq:*}

5. \cgn2_6/ptodata/1/\tilde{\text{Pubpna/USO6}} \text{NEW PUB.seq:*}

6. \cgn2_6/ptodata/1/\tilde{\text{Pubpna/USO6}} \text{NEW PUB.seq:*}

7. \cgn2_6/ptodata/1/\tilde{\text{Pubpna/USO8}} \text{NEW PUB.seq:*}

8. \cgn2_6/ptodata/1/\tilde{\text{Pubpna/USO8}} \text{PuBCOMB.seq:*}

9. \cgn2_6/ptodata/1/\tilde{\text{Pubpna/USO9}} \text{PuBCOMB.seq:*}

10. \cgn2_6/ptodata/1/\tilde{\text{Pubpna/USO9}} \text{PuBCOMB.seq:*}

11. \cgn2_6/\tilde{\text{Pubpna/USO9}} \text{PuBCOMB.seq:*}

12. \cgn2_6/\tilde{\text{Pubpna/USO9}} \text{Pubpna/USO9} \text{PuBCOMB.seq:*}

13. \cgn2_6/\tilde{\text{Pubpna/USO9}} \text{Pubpna/USO9} \text{PuBCOMB.seq:*}

14. \cgn2_6/\tilde{\text{Pubpna/USO9}} \text{Pubpna/USO9} \text{PuBCOMB.seq:*}

15. \cgn2_6/\tilde{\text{Pubpna/USO9}} \text{Pubpna/USO9} \text{Pubpna/USO8} \text{PuBCOMB.seq:*}

16. \cgn2_6/\tilde{\text{Pubpna/USO9}} \text{Pubpna/USO9} \text{PuBCOMB.seq:*}

17. \cgn2_6/\tilde{\text{Pubpna/USO9}} \text{Pubpna/USO9} \text{PuBcOMB.seq:*}

18. \cgn2_6/\tilde{\text{Pubpna/USO9}} \text{PuBCOMB.seq:*}

19. \cgn2_6/\tilde{\text{Pubpna/USO9}} \text{PuBCOMB.seq:*}

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19. \cgn2_6/\tilde{\text{Pubpna/USO9}} \text{PuBCOMB.seq:*}
     version 5.1.6
- 2004 Compugen Ltd.
                                                                           nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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       GenCore
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                                                                                                                                                41 LysArgAspSerValLysTrpHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsn
                                                                                                                                                                          LeuPheSerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePheAlaPheLys
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ASpThrValProAspAsnHisArgAsnLysPheLysValIleAsnValAspAspGly
                                                                                                                                                                                                                                                                                                   CysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGluIleMetGlnAsnAsnSerIle
                                                                       21 AsnGluLeuGlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27390, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
TITLE OF INVENTION: PROM VARIOUS cDNA LIBRARIES
FILE REPERBNCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
NUMBER OF SEQ ID NOS: 38054
SOCITARE FASTESC FOR WINDOWS VERSION 3.0
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Matches:
Conservative:
Mismatches:
Indels:
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) OTHER INFORMATION: n = A,T,C or US-09-918-995-27390
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264.50
84.72$
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NAME/KEY: misc_feature
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Best Local Similarity:
Query Match:
DB:
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US-09-918-995-27390
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ISEQUENCE 842, Application US/10276774

SEQUENCE 842, Application US/10276774

SEQUENCE 842, Application US/10276774

SEQUENCE 842, Application No. US20040053245A1

APPLICANT: Hyseq, Inc.

APPLICANT: Hyseq, Inc.

APPLICANT: Hyseq, Inc.

APPLICANT: Hyseq, Inc.

APPLICANT: Word Inc.

TATLE OF INVENTION: No. US20040053245A1e1 Nucleic Acids and Polypeptides

FILE REFERENCE: 21272-030

CURRENT APPLICATION NUMBER: US/560,875

PRIOR PLING DATE: 2000-04-27

PRIOR APPLICATION NUMBER: 09/496,914

PRIOR FILING DATE: 2000-04-27

NUMBER OF SEQ ID NOS: 2700

SOFTWARE: CUSCOM

SOFTWARE: CUSCOM

SEQ ID NO 842

LENGTH: 2074
                                                                                                                                                                                                                                                                                                                   96 AATGAGTTAGGTTCTGGCATAATGGAACTTACAGACACAGAACTGATTTTATACACCGCC 155
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                                                                                                                                                                                                                                             36 GACACTGTCCCAGATAACCATCGGAACAAGTTTAAGGTCATTAATGTGGATGATGGG
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                                                   Length:
Matches:
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ORGANISM: Homo sapiens
US-10-276-774-842
                                                                                         Percent Similarity:
Best Local Similarity:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 GlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArgLysArgAsp 43
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                                                                         APPLICANT: He, Yudong
APPLICANT: Lineley, Peter
APPLICANT: Maco Mao Mao Mao
APPLICANT: Roberts, Chris
APPLICANT: Van 't Veer, Laura
APPLICANT: Van de Viyver, Marc
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Vockley, Joseph G.
TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-757-415A-1_COPY_11_140 (1-130) x US-10-172-118-601 (1-1908)
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                              FILE REFERENCE: 9301-175-999
CURRENT APPLICATION NUMBER: US/10/172,118
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 601
LENGTH: 1908
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Publication No. US20040033502A1
GENERAL INFORMATION:
APPLICANT: Williams, Amanda
APPLICANT: Boland, Joseph F.
APPLICANT: Lord, Reginald V.
APPLICANT: Alvarez, Chris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NM 001381
DATABASE ENTRY DATE: 2001-06-18
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Lord, Reginald V.
Alvarez, Chris
Wetzel, Jon C.
Scherf, Uwe
US20030224374A1
                                                          Hongyue
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ATCAATGTGATGGAAGAGCCTGTCATCATCACCCGCAATAGCCACCCCGCTGAGCTTGAC 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Van de Vijver, Marc J.
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-188-999
CURRENT APPLICATION NUMBER: 0/298,918
FRICA APPLICATION NUMBER: 60/298,918
FRICA APPLICATION NUMBER: 60/380,710
FRICA RAPLICATION NUMBER: 60/380,710
FRICA FILING DATE: 2002-05-14
FRICA FILING DATE: 2002-06-14
FRICA RELING DATE: 2002-06-14
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                                                          119 ValProArgThrProArgThrProThrThrProGly 130
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Roberts, Christopher J.
Van 't Veer, Laura Johanna
Van de Vijver, Marc J.
                                                                                                                                                                                                                        Application US/10342887
). US20040058340A1
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143.50
47.32%
29.46%
20.62%
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APPLICANT: He, Yudong
APPLICANT: Linsley, Pet
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-10-172-118-601
                                                                                                                                                              RESULT 4
US-10-342-887-601
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Pred. No.: Score:

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2397 GGCTCCTACGTGCTGAGGGTGGAGGCTGAAAGGCTGACTCTCCTGACCGTGGGGGCCCAG 2456
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Patent No. US20020064855A1
GENERAL INFORMATION:
APPLICANT: Lemischka, Ihor
APPLICANT: Lemischka, Ihor
APPLICANT: MONOR, Kater THAT REGULATE HEMATOPIETIC BLOOD FORMING STEM
TITLE OF INVENTION: CELLS AND USES THEREOF
TITLE OF INVENTION: CELLS AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/789,919
CURRENT FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 96
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                                                             Length:
Matches:
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Query Match:
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Best Local Similarity:
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LENGTH: 1539
JS-10-001-870-68
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APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Macina, Roberto
APPLICANT: Bun, Vongming
APPLICANT: Sun, Yongming
APPLICANT: Lu, Chenghua
FILE REPERENCE: DEX-0283
FILE REPERENCE: DEX-0283
FILE REPERENCE: DEX-021-11-20
PRIOR APPLICATION NUMBER: 60/252,189
PRIOR APPLICATION NUMBER: 60/252,189
PRIOR APPLICATION NUMBER: 60/252,189
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patentin version 3.1
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| ACCITCCAGACGCACAGGGAAAIGACAICTICCAGGCAGTIGAGACIGCCAICCACCGG
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Matches:
Conservative:
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               CURRENT APPLICATION NUMBER: US/10/240,425
CURRENT FILING DATE: 2002-09-30
FRIOR APPLICATION NUMBER: PCT/USO1/09847
FRIOR FILING DATE: 2001-03-28
FRIOR FILING DATE: 2001-03-31
NUMBER OF SEQ ID NOS: 1588
SOFTWARE: Patentin Ver. 2.1
LENGTH: 1972
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Publication No. US20020150924A1
GENERAL INFORMATION:
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143.50
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29.46%
  REFERENCE: 44921-5026
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SEQ ID NO 68
LENGTH: 3809
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956 GAGCCCCCTGGAGGTTCGGGAGGTGGCCCCAGGATTTGAGCTGCCCACTCCCAGAAAG 1015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: No. US20030104529Alel Nucleic Acids and TITLE OF INVENTION: Polypeptides FILE REFERENCE: 784CIP2B
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Matches:
Conservative:
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PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SEQ ID NO 854
LENGTH: 1146
                                                                                     1016 CTGCCTCTAACTGATCCCGGG 1036
                                                                                                                                                                   Sequence 854, Application US/10037270 Publication No. US20030104529A1 GENERAL INFORMATION:
                                          125 ThrPro---ThrThrProGly 130
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137.50
49.07%
31.48%
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rei, hong
APPLICANT: Chen, Rui-hong
APPLICANT: Ahao, Qing A.
APPLICANT: Xue, Applicant: Xue, Addong J.
APPLICANT: Yang, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
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Wang, Zhiwei
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; LOCATION: (109)..(1122)
US-10-037-270-854
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Tillinghast,
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Ma, Yunging
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US-10-037-270-854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluProValValGluArgAsnAsnHisGlnThrGluLeuGluValProArgThrProArg 124
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                                                                                                           ArgalaGluGluLeuPheAsnMetLeuGlnGluIleMetGlnAsnAsnSerIleAsnVal 102
                                                                                                                                                                                                                                         785 CCAGAGCTGGCCATGTCCCCACCCTGCCCCTGCCTCGGGCCCTCTCCCTGCCCTGCCCTA 844
                                                                                                                                                                                                                                                                                 GluProValValGluArgAsnAsnHisGlnThrGluLeuGluValProArgThrProArg 124
                                                                                                                                                                                                                                                                                                                         845 GAGCCCCTGGAGACTTCGGGAGGTGGCCCCCAGGATTTGAGCTGCCCACTCCCAGAAAG 904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 57, Application US/09789919

Sequence 57, Application US/09789919

Sequence 57, Application US/09789919

GENERAL INFORMATION:

APPLICANT: Lenischka, Ihor

APPLICANT: Moore, Kateri

TITLE OF INVENTION: GENES THAT REGULATE HEMATOPIETIC BLOOD FORMING STEM

TITLE OF INVENTION: GENES THAT REGULATE HEMATOPIETIC BLOOD FORMING STEM

FILLE REFERENCE: 2275-1-005

CURRENT APPLICATION NUMBER: US/09/789,919

CURRENT APPLICATION NUMBER: US/09/789,919

NUMBER OF SEQ ID NOS: 96

SOFTWARE: Patentin Ver. 2.0
                          SerPheGluSerGlyArgArgCysGlnThrGlyGlnGlyIlePheAlaPheLysCysAla
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Matches:
Conservative:
Mismatches:
Indels:
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44.09%
28.35%
20.26%
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                                                                                                                                                                                              103 ValGlu----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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853 ACAAGCTTGACTGAACCAATGACA 876
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LENGTH: 17
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                                                     -- ProValValGluArgAsnAsnHisGln 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 CysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGluIleMetGlnAsnAsnSerIle 100
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                                                                                                                                                                                                                                                                                                                            APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030219744Alel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 7847P2ECTP
CURRENT APPLICATION NUMBER: US/10/117,722
CURRENT PILING DATE: 2002-04-04
PRIOR FILING DATE: 2000-07-19
PRIOR PELING DATE: 2000-07-19
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/582,317
PRIOR FILING DATE: 2000-04-25
PRIOR PRILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR PRILING DATE: 2000-01-21
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Matches:
Conservative:
Mismatches:
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                                                                                                                   ThrGluLeuGluValProArgThr 122
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Publication No. US20030219744A1
GENERAL INFORMATION:
                                                                                                                                                                 853 ACAAGCTTGACTGAACCAATGACA
                    101 AsnValValGluGlu------
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49.07%
31.48%
19.76%
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; LOCATION: (109)..(1122)
US-10-117-722-854
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ORGANISM: Homo sapiens
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Best Local Similarity:
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SEQ ID NO 854
LENGTH: 1146
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Pred. No.:
                                                                                                                   115
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TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS TITLE OF INVENTION: THE SAME FILE REPERENCE: 24102-502D
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NUMBER OF SEQ ID NOS: 53
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Mismatches:
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PRIOR APPLICATION NUMBER: 60/341,477
PRIOR FILING DATE: 2001-12-17
PRIOR PELING DATE: 2001-12-17
PRIOR PELING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/342,592
PRIOR APPLICATION NUMBER: 60/343,983
PRIOR PILING DATE: 2001-12-20
PRIOR PELING DATE: 2001-12-31
PRIOR PELING DATE: 2002-04-17
PRIOR PELING DATE: 2002-04-17
PRIOR PELING DATE: 2002-05-18
PRIOR APPLICATION NUMBER: 60/391,495
PRIOR APPLICATION NUMBER: 60/391,495
PRIOR FILING DATE: 2002-05-17
PRIOR PELING DATE: 2002-05-18
PRIOR PELING DATE: 2002-05-28
PRIOR FILING DATE: 2002-05-28
PRIOR FILING DATE: 2002-05-28
PRIOR PILING DATE: 2002-05-28
PRIOR PILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 60/391,744
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: 60/391,749
PRIOR PILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: 60/391,749
PRIOR APPLICATION NUMBER: 60/391,749
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PRIOR APPLICATION NUMBER: 60/391,749
PRIOR APPLICATION NUMBER: 60/391,749
PRIOR APPLICATION NUMBER: 60/391,749
PRIOR FILING DATE: 2002-05-29
RESULT 12
US-10-307-928A-5
Sequence 5, Application US/10307928A
Spublication No. US20030229016Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                          Edinger, Shlomit R.
Gorman, Linda
Guo, Xiaojia (Sasha)
                                                                                                                                                                                                                                    Boldog, Ferenc L.
Burgess, Catherine
                                                                                                                                                                                                                                                                                                Catterton, Elina
Edinger, Shlomit R.
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                                                                                                                                                                                                        Anderson, David W.
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Voss, Edward Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ıtturajan, Meera
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; LOCATION: (197)..(1189)
US-10-307-928A-5
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685 IGGIICACGIIIGAGATCAGGAAGAAIGIGIGACAGGAAGAAGAACATTTCAA 744
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                                                                                                                      576 AATOCCCCCCCCCCCCCCCCCCCCCCCTACTCTCGCCCCCATGACTCACTGCC 635
   --CAGCCAGCCAC 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 GlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArgLysArgAsp 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44 ServalLys-----TrpHisTyrLeuCysLeuArgArgTyrGlyTyrAgpSerAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tillinghast, John
APPLICANT: Drmanac, Radoje T.
ITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
TITLE OF INVENTION: PolyPeptides
FILE REFERENCE: 784CIP2B
GURRENT APPLICATION NUMBER: US/10/037,270
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: PL_LGenes Version 1.0
SEQ ID NO 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-757-415A-1_COPY_11_140 (1-130) x US-10-037-270-855 (1-914)
528 IGCCCAGAAGAAIGCIGCACCCGCIACACCCCAACCG----
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                          636 GCCGCCTTCACCCACACAC 657
                                                                                                                                                                                                                                                                                                                                US-10-037-270-855; Sequence 855, Application US/10037270; Publication No. US20030104529A1; GENERAL INFORMATION:
                                                                   114 nThrGluLeuGluValProArg
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1133.50
48.62%
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APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Zhang, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Chen, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Zhao, Qing A.
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Wang, Jian-Rui
Zhou, Ping
Ma, Yunging
Wang, Dunrui
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Xue, Aidong
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: (109)..(867)
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Best Local Similarity:
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APPLICANT: Dotson, Stanton B.
APPLICANT: Dotson, Stanton B.
APPLICANT: Dotson, Stanton B.
APPLICANT: Dotson, Stanton Wileic acid, polypeptides, vectors, and cells derived from activ TITLE OF INVENTION: eosinophil cells
FILE OF INVENTION: Eosinophil cells
FILE REFERENCE: S03157-01
GURRENT APPLICATION NUMBER: US/10/350,923B
CURRENT PILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: DS/09/28773
PRIOR FILING DATE: 1999-66-12
PRIOR FILING DATE: 1999-66-12
PRIOR FILING DATE: 1999-12-04
NUMBER OF SEQ ID NOS: 79-12-04
NUMBER OF SEQ ID NOS: 79-12-04
SSCTARRE: PACENTANE DELICATION NUMBER: DS/09/28773
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      713 paggichahaciggigangiggcererengerekingkagakarackingkang 772
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                                                                                                      44 SerVallys-----TrpHisTyrLeuCysLeuArgArgTyrGlyTyrAspSerAsn
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Matches:
Conservative:
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Indels:
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Query Match:
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US-10-350-923B-37
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81 CysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGluIleMetGlnAsnAsnSerIle 100
                         101. ASHValValGluGluProValValGluArgAshAshHisGlnThrGluLeuGluValPro 120
                                                                                                      81 CysAlaArgAlaGluGluLeuPheAsnMetLeuGlnGluIleMetGlnAsnAsnSerIle 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 GlySerGlyIleMetGluLeuThrAspThrGluLeuIleLeuTyrThrArgLysArgAsp 43
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                                                                                                                                                                                                                                                                                                                              APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Annud, Vinod
APPLICANT: Annud, Vinod
APPLICANT: Annung, Jie
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
CURRENT APPLICATION NUMBER: US,10/117,722
CURRENT APPLICATION NUMBER: US,002-04-04
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Matches:
Conservative:
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Indels:
Gaps:
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PRIOR PLICATION NUMBER: 09/620,312

PRIOR FILING DATE: 2000-07-19

PRIOR FILING DATE: 2000-07-19

PRIOR FILING DATE: 2000-04-25

PRIOR FILING DATE: 2000-01-21

PRIOR FILING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 1104

SOFTWARE: DE FL_Genes Version 1.0

SEQ ID NO 855

LENGTH: 914

TYNDE: ...
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US-10-117-722-855
US-10-117-722-855

Sequence 855, Application US/10117722
Publication No. US20030219744A1
GENERAL INFORMATION:
                                                                                                                793 GCCATAGCTGAGCAA-----
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133.50
48.62%
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NAME/KEY: CDS
LOCATION: (109)..(867)
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Best Local Similarity:
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sw model protein search, using protein δ

August 2, 2004, 09:22:38; Search time 13.8947 Seconds (without alignments)
447.367 Million cell updates/sec Run on:

US-09-757-415A-3

1 HSQMAVHKLAKSIPLRRQVTVS 22 Title: '' Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 Total number of hits satisfying chosen parameters:

1586107 segs, 282547505

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s: *
geneseqp2001s: *
geneseqp2002s: *
geneseqp2003as: * geneseqp2003bs:* A_Geneseq_29Jan04:* geneseqp1990s:* geneseqp1980s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

	ion	1	Mouse fib	Tumour in	Chicken b	Human bFG	Lung canc		Human fib	-		Amino aci		flg recep	Em.	Mouse	Human	Human Fib	Rat	Rat Prote		Chicke	Clone pTB	Human Pro	Murine KG		Clor
	Description		. Aau04695	Abg79680	Aar10649	Aar21686	Aab58376	Aar39647	-Aar47233	Aaw63844	Aay06458	Aab84383	Aar13549	Aar20750	Aar26337	Aau04694	- Aae34488	Abr56164	Ade61698	Ade55803	Ade61700	Aar10648	Aar15267	Add47011	Aar14280	Aar10933	Aar15268
SUMMARIES	ID		AAU04695	ABG79680	AAR10649	AAR21686	337	AAR39647	AAR47233	AAW63844	AAY06458	AAB84383	AAR13549	AAR20750	AAR26337	AAU04694	AAE34488	ABR56164	ADE61698	ADE55803	ADE61700	AAR10648	AAR15267	ADD47011	AAR14280	AAR10933	AAR15268
	DB	1	4,	S	7	7	m	7	7	~	7	4	7	0	~	4	9	~	7	7	7	N	7	7	N	0	7
	Length		22	702	731	731	764	816	820	820	820	820	822	822	822	822	822	822	822	822	822	819	643	654	726	726	769
ak	Query Match		100.0	100.0		100.0		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	00	90.7	۲.		77.6	۲.	77.6
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Aar21080 flg recep	Ade57113 Human Pro	Add45446 Human Pro	Aaw37804 Fibroblas	Aay23631 Bek-like	Aay23633 Newt kera	Aaw37806 Keratinoc	Aar15266 Clone pTB	Aar15269 Clone pTB	Aar41517 K-sam. 3/	Abr98369 Tumour ce	Adc84715 MCF-7 bre	Abg29386 Novel hum	Aae34390 Human per	Aab31889 Amino aci	Abg23265 Novel hum		Aag89977 C glutami		Abu23813 Protein e
AAR21080	ADE57113	ADD45446	AAW37804	AAY23631	AAY23633	AAW37806	AAR15266	AAR15269	AAR41517	ABR98369	ADC84715	ABG29386	AAE34390	AAB31889	ABG23265	ABG23262	AAG89977	ADC86177	ABU23813
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9.1	9.	9.1	5.7	5.7	۲.	5.7	6.4	6.4	6.4	8.8	8.6	46.7	6.8	6.8	43.9	43.0	41.1	1.1	.2
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83	83	83	81	81	81	81	71	71	71	64	64	20	47	47	47	46	44	44	43
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26	27	28	59	30	31	32	33	34	35	36	37	38⊹	9	40	41	42	43	44	45

ALIGNMENTS

AAU04695 standard; peptide; 22 AA. RESULT 1 AAU04695

AAU04695;

entry) (first 26-SEP-2001

Mouse fibroblast growth factor receptor-1 (FGFR1)-derived peptide.

FGFR; Suc-1-associated neurotrophic factor target protein; SNT-1; protein co-ordinate data; mouse; fibroblast growth factor receptor; nuclear magnetic resonance; NMR spectroscopy; rational drug design; three-dimensional structure.

Mus musculus.

WO200151521-A2.

19-JUL-2001.

10-JAN-2001; 2001WO-US000821.

12-JAN-2000; 2000US-0175867P. 09-JAN-2001; 2001US-00757415.

(MOUN) MOUNT SINAI SCHOOL MEDICINE.

Zhou M;

WPI; 2001-425868/45.

New isolated nucleic acid sequences encoding polypeptides useful in structure based rational drug design.

Claim 11; Page 44; 235pp; English.

The sequence represents the amino acid sequence of mouse fibroblast growth factor receptor-1 (FGFR1)-derived peptide. The invention provides fragments of suc-1-associated neurotrophic factor target protein (SNT) and fibroblast growth factor receptor (FGFR) which can form a binding complex that is amenable to structural determinations by nuclear magnetic resonance (NMR) spectroscopy. The invention provides methodology for related structure based rational drug design using the three-dimensional data. The invention fulfills the need for the determination of the three-dimensional structure of such complexes as described and for procedures for related structural base drug design predicated on such structural

RESULT 2 ABG79680

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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
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                                                                                                                                                                                   Sequence 702 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUL-1989;
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17-APR-1991
                                                                                                                                                disclosed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention discloses isolated human nucleic acid alternative splicing variants that are all tumour-involved genes (TIGS). The nucleic acids and CV variants that are all tumour-involved genes (TIGS). The nucleic acids and CV polypeptides are useful for determining the level of a nucleic acid or polypeptide sequence in a biological sample, for determining the level of variant nucleic acid or polypeptide sequences in a biological sample and for determining the ratio between the level of variant sequence in a first biological sample and the level of the original sequence from which composition comprising a carrier and the nucleic acid, is useful for composition comprising a carrier and the nucleic acid, is useful for treating diseases (e.g. cancer) that can be ameliorated or cured by increasing or decreasing the level of the encoded protein. The nucleic acids are also useful for diagnostic purposes, especially for detecting cancer or a precisposition to cancer, for evaluating the state or aggressiveness of cancer disease, in basic research, for understanding the physiological function of the original TIG, in targeting or developing pharmaceuticals, for distinguishing various stages in the life
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acid sequence, which is an alternative splicing variant of tumor involved genes, useful for detecting cancer, predisposition to cancer, for evaluating cancer state and in gene therapy for treating
                                                                                                                                                                                                                                                                                                                                                                                                          Human, splice variant, tumour-involved gene; TIG;
pharmaceutical composition, cancer; diagnostic, tumour; gene therapy;
endothelial cell; cell differentiation, cell proliferation; apoptosis;
                                                                                         ő
                                                                                                                                                                                                                                                                                                                                                                        Tumour involved gene (TIG) splice variant protein, NV-11.
                                                    / Match 100.0%; Score 107; DB 4; Local Similarity 100.0%; Pred. No. 1.9e-11; nes 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 76-77; 180pp; English.
                                                                                                                              1 HSQMAVHKLAKSIPLRRQVTVS 22
                                                                                                                                                                                                                                                           ABG79680 standard; protein; 702 AA.
                                                                                                                                                               1 HSQMAVHKLAKSIPLRRQVTVS 22
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16-MAY-2000; 2000IL-00136154.
                                                                                                                                                                                                                                                                                                                                   15-NOV-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DAVI/) DAVID A.
(ROMA/) ROMANO C.
(BERN/) BERNSTEIN J.
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N-PSDB; ABS65210.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LEVI/) LEVINE Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2002086384-A1.
                     Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy
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                                                        Query Match
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(ROMA/)
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oycle of the same type of cells which may be helpful for the development of pharmaceuticals for various cancer stages in which cell cycle is non-normal, for determining mutations in tumour-involved genes and in gene therapy. The polypeptides are useful for identifying compounds capable of binding to the variant product and modulating its activity and for modulating endochelial differentiation and proliferation, as well as to modulate apoptosis either ex vivo or in vivo. The sequences presented in ABG796700-ABG79705 are the new variants (NV) 1-16 proteins of the TIGs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Best Local Similarity 100.0%; Pred. No. 1e-09;
Matches 22; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      409 HSOMAVHKLAKSIPLRROVIVS 430
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99US-0124270P.

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Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as lung cancer.
                                                                                                                                                                                                                                                                                                                 Claim 11; Page 1225-1228; 1425pp; English.
                                                                       08-MAR-2000; 2000WO-US005918.
                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                            WPI; 2000-587514/55
                                                                                                                                                 (ROSE/) ROSEN C A.
                                                                                                                                                                                                                            N-PSDB; AAF18252
               WO200055180-A2
                                                                                                      12-MAR-1999;
                                         21-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human b-FGF receptor gene - contains recombinant DNA, chromosome DNA or cDNA base sequence encoding polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The human basic fibroblast growth factor (D-FGF) receptor protein sequence was deduced from the DNA sequence obtd. from a human placenta cDNA library in lambda gill. The library was screened with two probes (AAQ24634.5) which were derived from the known FLG sequence (fms like gene). Positive clones were transformed into E. coli Y1090 strain, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                               Basic fibroblast growth factor; fms like gene
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                                      318 HSQMAVHKLAKSIPLRRQVTVS 339
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                   HSOMAVHKLAKSIPLRRQVTVS 22
                                                                                                                         AAR21686 standard; protein; 731 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 2; 10pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                               (MITK ) MITSUI TOATSU CHEM INC
                                                                                                                                                                                                                                                                                                                                                                  90JP-00141490
                                                                                                                                                                                                                                                                                                                                                                                                  90JP-00141490
                                                                                                                                                                                                                 Human bFGF receptor protein
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                                                                                                                                                                                  03-JUL-1992
                                                                                                                                                                                                                                                                             Homo sapiens
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Polymucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AABS8106 - AABS8548. Lung cancer associated proteins and polymucleotide sequences, their agonists, and cartering and polymucleotide sequences, their agonists, and general included in the confidential cartiological; cardioactive; and munomodulatory; muscular active general; vilnerary; gastrointestinal cereivity. The invention also includes antibodies specific for the protein atoinculates antibodies specific for the protein or polymucleotide sequences. The lung cancer associated polymucleotide sequences may be used for detection of lung cancer, chromosome content and proteins may be used to treat disorders such as cereiovascular, reproductive, astrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases.

Company of the polymucleotide and protein and peptide AABS549 are used in the course of the invention for the identification and characterisation of the polymucleotide and protein sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 soluble, FGF-R; fibroblast growth factor receptor; tumour therapy; immunoglobulin-like domain; tyrosine kinase activity; hyperplasia; psoriasis; Herpes Simplex Virus; HSV.
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/note= "putative signal peptidase site"
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/label= Ig-like_domain_1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 764 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR39647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local 8
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sapiens

Homo

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Homo sapiens

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0
126. .133
/label= ARR
/label= ARR
137. .143
/note= "acidic amino acid rich region"
170. .143
/note= "the sequence EEKKEKE in Seq.ID.No.1 is shown as EEKE in Fig. 2"
/label= Ig-like_domain-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention covers both the full-length FGF-receptor and its soluble form (i.e. truncated by deletion of the C-terminal portion beginning at the transmembrane domain). The FGF receptor is defined as having the sequence in Columns 13-18 and Fig 2. These sequences differ slightly as indicated by the "Misc difference" in the Features Table. The receptor can be used to detect FGF or to inhibit FGF activity. Specifically, the soluble form of the receptor can inhibit FGF-dependent tumour growth, anglogenesis, psoriasis, excessive scar formation and hyperplasias and can be used to treat Herpes Simplex virus infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant human fibroblast growth factor receptor - is useful in treatment of hyperplasia(s), tumours and herpes simplex infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                     /label= Tyrosine Kinase_domain
/note= "second part of split TK domain"
                                                                                                                                                                            175. 575
Tabel= Tyrosine Kinase domain
Mote= "first part of split TK domain"
8500. 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
100.0%; Score 107; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 2 and Columns 13-18; 21pp; English.
                                                                                                                                  Ig-like_domain-3
                                                                                                                                                 772. .392 Tabsmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                 Barr PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         404 HSQMAVHKLAKSIPLRRQVTVS 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR47233 standard; protein; 820
                                                                                                                                                                                                                                                                                                                                            91US-00640029
                                                                                                                                                                                                                                                                                                                                                                        91US-00640029
                                                                                                                                                                                                                                                                                                                                                                                                                               Valenzuela PDT,
                                                                                                                    278. .341
/label= Ig
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1993-242535/30.
                                                                                                                                                                                                                                                                                                                                                                                                   (CHIR ) CHIRON CORP
                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 816 AA;
                                                                                                                                                                                                                                                                                                                                          11-JAN-1991;
                                                                                                                                                                                                                                                                                  US5229501-A
                                                                                                                                                                                                                                                                                                                                                                                                                                 Keifer MC,
    Region
                                                                                      Domain
                                                                                                                    Domain
                                                                                                                                                 Domain
                                                                                                                                                                             Domain
                                                                                                                                                                                                                          Domain
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AAR47233
ID AAR4
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178. .578
| Jabel = TK
| Incte = "first part of split intracellular tyrosine kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expression of recombinant viral glycoproteins on host cell surfaces can be significantly enhanced by coexpression with an escort protein. The CMV glycoprotein H polypeptide (see AAR47222) is a preferred viral receptor. See AAR47221) is a preferred viral receptor. A full-length FGF receptor CDNA, designated fl95, was isolated from a lambda ZAP human hepatoma HepG2 CDNA library; flg5 codes for a 820 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Increased expression and secretion of viral protein e.g. from cytomegalovirus from host cells - by co-expression with DNA encoding an escort protein, e.g. fibroblast growth factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                         593. 754
/label= TK
hote="second part of split intracellular tyrosine
kinase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                label= ARR
note= "acidic amino acid-rich region"
176. .23
label= immunoglobulin-like_domain_2
                                                                                   label= immunoglobulin-like_domain_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 107; DB 2;
100.0%; Pred. No. 1.2e-09;
ive 0; Mismatches 0;
                                                                                                                                                                                                            note= "extracellular"
74. 395
label= transmembrane_domain
                                                                2. .820
label= human_FGF_receptor
                                                      label= signal_peptide
                                                                                                                                                                            note= "extracellular"
75. .339
                                 location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
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                                                                                                                                                                                                                                                                                                                                                                                           93WO-US007299.
                                                                                                                                                                                                                                                                                                                                                                                                                  92US-00921807,
                                                                                                                       .133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                               domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 820 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                           29-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                 WO9403620-A2
                                                                                                                                                                                                                                                                                                                                                                    17-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spacte RL;
                                 Key
Peptide
                                                                Protein
                                                                                       Domain
                                                                                                                       Region
                                                                                                                                                        Domain
                                                                                                                                                                                        Domain
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RESULT 8 AAW63844

407 HSQMAVHKLAKSIPLRRQVTVS 428

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Cytomegalovirus, CMV, Towne, gH gene, escort protein, recombinant protein production, viral glycoprotein H, FGF receptor, fibroblast growth factor receptor, soluble, flg5 cDNA clone.

XXXEXXEXXEX,

Human fibroblast growth factor receptor.

(revised) (first entry)

25-MAR-2003 07-SEP-1994

AAR47233;

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The present sequence represents human fibroblast growth factor receptor 1 (FGFR1), which is encoded by a gene on human chromosome 8. A newly can dentified oncogene, STRT98 FCFR1 (see AAX80177), incorporates a FGFR1 tyrosine kinase domain fused through t (8,13) translocation to ZNF198, a cover zinc finger protein (see AAY66457) and is associated with stem cell conceptual and the encoded oncoprotein (see AAY66456) provides the ability conceptual and the encoded oncoprotein (see AAY66456) provides the ability conceptual and the encoded oncoprotein (see AAY66456) provides the ability conceptual conceptual states and propes capable of hybridizing to ZNF198 or FGFR1 tyrosine kinase and probes capable of hybridizing to ZNF198 or FGFR1 tyrosine kinase domain coding sequences. Cells containing ZNR198 FGFR1 can be located using a radiolabeled antibody that recognizes the fusion juncture locus.

Antibodies that recognize this fusion juncture can also be used to deliver toxic substances to patients containing the ZNF198 FGFR1 protein.
                                                                                              ZNF198-FGFR1; fibroblast growth factor receptor 1; oncogene; lymphoma; leukaemia; SCLL; translocation; stem cell; diagnosis; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oncogene, designated ZNP198-FGFR1, useful in diagnosis of stem cell leukemia and lymphoma syndrome.
                                                                                                                                                                                     426. .427
/note= "translocation breakpoint"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 70-72; 76pp; English
                                                                    Fibroblast growth factor receptor 1.
                                                                                                                                                                                                                                                                                                                                                                               (BGHM ) BRIGHAM & WOMENS HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                   98US-00004688.
                                                                                                                                                                                                                                                                                                                       99WO-US000365
                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                            Fletcher JA, Xiao S;
                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-430381/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAX87179
                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                              WO9935159-A1
                                                                                                                                                                                                                                                                                                                       07-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                   08-JAN-1998;
                                         27-SEP-1999
                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                          15-JUL-1999
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             AAY06458
                                                                                                                                                                                                                      Domain
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a murine basic fibroblast growth factor (bFGF) which is a member of the heparin-binding growth factor receptor family. This protein is used in a method which assays the ability of a substance to bind to a high-affinity heparin-binding growth factor (HBGF) receptor. The assay screens for potential anti-umour agents that inhibit binding of HBGF to high-affinity receptors, or for potential wound healing agents that promote such binding. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assays for high-affinity heparin-binding growth factor receptor ligands using receptor-overexpressing cells or cell-free system.
                                                                                                                             Basic fibroblast growth factor receptor; bFGF; heparin binding; murine; antitumour agent; inhibitor; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 820;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klagsbrun M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 107; DB 2; Length 8
100.0%; Pred. No. 1.2e-09;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ornitz DM,
                                                                                                                                                                                                      Location/Qualifiers
 AAW63844 standard; protein; 820 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leder P, Yayon A, Flanagan JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 9; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                  label= unknown
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                                                                                                                                                                                                                                  label= unknown
                                                                                                                                                                                                                                                               label= unknown
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                                                                                                                                                                                                                                                                                                                       label= unknown
                                                                                                                                                                                                                                                                                                                                                     label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HARD ) HARVARD COLLEGE.
(CHIL-) CHILDRENS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90US-00631717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93US-00166717
                                                                                                    receptor protein.
                                                         (revised)
(first entry)
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Best Local Similarity Love.
22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-446074/38.
N-PSDB; AAV44041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 820 AA;
                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                       Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-AUG-1998.
                                                       25-MAR-2003
01-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                            JS5789182-A.
                                                                                                 Mouse bFGF
                             AAW63844;
                                                                                                                                                                          Mus sp.
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/note= "tyrosine kinase domain I"

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Location/Qualifiers

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0
                                          Gaps
                                          ö
                   Length 820;
                                          Indels
                   100.0%; Score 107; DB 2; 100.0%; Pred. No. 1.2e-09;
                                        Mismatches
                                                                                    407 HSQMAVHKLAKSIPLRRQVTVS 428
                                                               22
                                                                                                                                           AAB84383 standard; protein; 820 AA.
                                                                1 HSOMAVHKLAKSIPLRROVTVS
                                          ..
0
                                                                                                                                                                                      (first entry)
                             Local Similarity 100.
Sequence 820 AA;
                                                                                                                                                                                      22-AUG-2001
                                                                                                                                                                 AAB84383;
                                                                                                                      RESULT 10
                                                                                                                                 AAB84383
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Gaps .; 0

HSQMAVHKLAKSIPLRRQVTVS 428

407

8 g

HSQMAVHKLAKSIPLRRQVTVS

AAY06458 standard; protein; 820 AA.

AAY06458 ID AAY0 RESULT 9

used to

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The sequence was deduced from the cDNA sequence obtd. from two overlapping clones, PL5 and PL10, isolated from a placental lambda gtll cDNA library. The DNA can be used to express recombinant bRGF receptor which is an antagonist of human aRFGF and bRGF. The receptor can be used to treat abnormal anglogenesis (e.g. in diabetic retinopathy, neovascular glaucoma, etc., and possibly certain solid tumours), and in contraceptives. Dosage is 10-100 ug. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                               Extracellular form of human fibroblast growth factor receptor treat tumours, abnormal angiogenesis e.g. diabetic retinopathy, rheumatoid arthritis and arteriosclerosis and as contraceptives
                                                                                                                                   Sarmientos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fibroblast growth factor receptor, heparin binding proteins, tyrosine kinase, fms-like gene, CSF-1, PDGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185
/note= "N-linked glycosylation site"
                                                                                                                                   Roncucci R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 107; DB 2;
ilarity 100.0%; Pred. No. 1.2e-09;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22. .822
/label= flg_receptor_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . .21
|abel= signal_peptide
                                                                                                                                 Isacchi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  409 HSQMAVHKLAKSIPLRRQVTVS 430
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                                                                                               (FARM ) FARMITALIA ERBA SRL CARLO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 HSQMAVHKLAKSIPLRRQVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR20750 standard; protein; 822
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                                                                                                                                                                                                                                                                                    Claim 1; Fig 3; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90US-00549587.
                                 90GB-00001466
                                                                 90GB-00001466
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(first entry)
                                                                                                                                   Bergonzoni L, Mazue G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            flg receptor protein.
                                                                                                                                                                 WPI; 1991-252611/34.
N-PSDB; AAQ13311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 822 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                 23-JAN-1990;
                                                                 23-JAN-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
20-MAY-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a human fibroblast growth factor receptor (FGFR). FGFR is useful for detecting FGF in a sample, and for inhibiting the activity of FGF. The FGFR may also be used to screen and identify compounds which mimic FGF binding: FGFR can be used to identify agonists and antagonists. The agonists identified may be used to accelerate wound healing, and the antagonists identified can be used to inhibit the growth of FGF-related malignancies
                                                                                                                                                                                                                                                                                                                                                                                    Novel fragment of a human fibroblast growth factor receptor, used to detect fibroblast growth factor in samples and to identify modulators of the factor, which are used to accelerate wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                               Human; fibroblast growth factor receptor; FGFR; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 107; DB 4; Length 820; Pred. No. 1.2e-09;
sequence of a fibroblast growth factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22. .822
/label= mat_peptide
22. .376
/label= extracellular_portion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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/label= signal_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Basic fibroblast growth factor; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSQMAVHKLAKSIPLRRQVTVS 428
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                                                                                                                                                                                                                 91US-00640029.
93US-00046020.
94US-00315686.
                                                                                                                                                                                   95US-00439992.
                                                                                                                                                                                                                                                                                                                      Valenzuela PDT,
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(first entry)
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22; Conservative

Matches

à g

407

RESULT 11

Basic FGF receptor.

25-MAR-2003 28-OCT-1991

AAR13549;

Homo sapiens

Peptide Protein Region WO9111459-A.

Local Similarity

Query Match

Sequence 820 AA;

WPI; 2001-388930/41.

Keifer MC,

(CHIR) CHIRON CORP.

12-APR-1993; 30-SEP-1994;

11-JAN-1991;

US6255454-B1

Homo sapiens

malignancy

acid

12-MAY-1995;

03-JUL-2001

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Gaps

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The sequence given encoded by the N-sam tumour gene. This protein could be the receptor of human bFGF. The N-sam protein and peptide fragments of N-sam are useful as anti-tumour drugs. Anti-N-sam peptide antibodies are useful for the detection of the N-sam gene product, in the purification of the N-sam gene product and in the diagnosis of tumours and anti-tumour
          Claim 1; Fig 1; 19pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 822 AA;
                                                                                                                                   Sequence 822 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus.
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Local Sim.
22;
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                                                                                                                                                                                                                                                                                                                                           AAU04694;
                                                                                                                                                            Query Match
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                                                                                                         drugs
                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                            g
                                                                                                                                         The protein sequence was deduced from the DNA sequence of an flg cDNA clone having increased binding for aFGF receptors. Flg and bek are clone having increased binding for aFGF receptors. Flg and bek are clone having increased binding for aFGF receptor. Inked tyrosine kinases. They have a DDGF/CSF-1/C-kit family of receptor linked tyrosine kinases. They have a cc 21 residue hydrophobic signal sequence, flg has an extracellular domain of 355 residuees. They can actidic box of 8 anino acids in the Cytoplasmic domains of similar carracellular domain contains 3 "immunoglobulin like" domains of similar size and location. There are nine potential N-glycosylation sites. There is an "acidic box" of 8 anino acids. The Cytoplasmic domains of similar complexes and location. There are nine potential N-glycosylation sites. There is an "acidic box" of 8 anino acids. The Cytoplasmic domains of similar complexes completed in a partial seceptor proteins encoded by this collowed by acquence may be used in plarm- accultical compens. to inhibit undesirable responses may be growth factor mediated cellular responses or to inhibit responses may be growth factor stimulated angiogenests and vascularisation of tumours, mitogenic effects in psoriasis, arthritis, atherents and also be used for screening drugs for treatment of such problems. See also AAR21080 (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ·,
                                                                  New fibroblast growth factor receptor proteins - useful in treating gf-mediated conditions e.g. angiogenesis of tumours, mitogenic effects in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene prod of N-sam tumour - and its recombinant-contg. nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 107; DB 2; 100.0%; Pred. No. 1.2e-09; No. Mismatches 0;
 Schlessing J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSOMAVHKLAKSIPLRROVTVS 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 HSQMAVHKLAKSIPLRRQVTVS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR26337 standard, protein, 822 AA.
Jaye MC,
                                                                                                                        Claim 5; Fig 7; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90JP-00316100,
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(KOKU-) KOKURITSU GAN CENT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
nes 22; Conservative
 Crumley G,
                                                                                            psoriasis, arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-280111/34.
N-PSDB; AAQ27658.
                           WPI; 1992-056827/07
                                         N-PSDB; AAQ21003
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 822 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP04190792-A
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 Dionne CA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR26337;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suc-1-associated neurotrophic factor target protein; SNT-1; protein co-ordinate data; mouse; fibroblast growth factor receptor; FGFR; nuclear magnetic resonance; NMR spectroscopy; rational drug design; three-dimensional structure.
                                                                    Gaps
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                                                                    Indels
   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse fibroblast growth factor receptor-1 (FGFR1).
100.0%; Score 107; DB 2; 100.0%; Pred. No. 1.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Page 230-233; 235pp; English.
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                                                                                                                                                                                                       409 HSQMAVHKLAKSIPLRRQVTVS 430
                                                                                                                                  22
                                                                                                                                                                                                                                                                                                                                                                                  AAU04694 standard; protein; 822 AA
                                                                                                                                         1 HSOMAVHKLAKSIPLRROVTVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JAN-2000; 2000US-0175867P. 09-JAN-2001; 2001US-00757415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-425868/45.
                                Similarity
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Gaps .; 0 0; Indels Pred. No. 1.2e-09; Mismatches 0; 409 HSOMAVHKLAKSIPLRROVTVS 430 22 AAE34488 standard; protein; 822 AA 100.0%; Pre 1 HSQMAVHKLAKSIPLRRQVTVS 14-MAY-2003 (first entry) Best Local Similarity 100. Matches 22; Conservative Human FGF-R1 protein. AAE34488;

Human, pyridylpyrimidine derivative, cellular protein kinase, Scrapie, cellular protein protein posphylaxis, preliular signal transduction; prophylaxis, prion infection; chronic wasting disease; CWD; Creutzfeldt-Jacob disease, CJD, transmissible mink encephalopathy; bovine spongiform encephalopathy; transmissible mink encephalopathy; bovine spongiform encephalopathy; MTE, SSE, Gerstemann-Straussler-Scheinker syndrome; GSS, Alpers syndrome; fatal familial insomnia; FPI; kuru; neurodegenerative disease; nootropic; Alzheimer's disease; RGF-RI; flg; FI-1; FIt-2; b-FGFR.

Homo sapiens,

WO200293164-A2.

21-NOV-2002

16-MAY-2002; 2002WO-EP005420

16-MAY-2001; 2001EP-00111858. 29-MAY-2001; 2001US-0293E38P. 13-UUL-2001; 2001US-0305898P. 18-UUL-2001; 2001US-0305899P.

(AXXI-) AXXIMA PHARM AG.

Stein-Gerlach M, Salassidis K, WPI; 2003-120714/11. N-PSDB; AAD52780.

Bacher G, Mueller S;

New pyridylpyrimidine derivatives useful in the treatment or prevention of infectious disease e.g. Kuru syndrome and Creutzfeld-Jacob disease

Disclosure; Page 63-65; 96pp; English.

The invention relates to novel pyridylpyrimidine derivatives and methods of detecting prion infections and/or prion disease in an individual or in cells, cell cultures and/or cell lysates. The method involves adding at least one monoclonal or polyclonal antibody, oligonucleotide or pyridylpyrimidine derivative to the sample or in cells, cell cultures and/or cell lysates and detecting the activity of at least one human cellular protein kinases (e.g., FGF-R1 (also known as flg, Fl-1, Flt-2, b-FGFR), Tkt (also known as c-abl), clk1, MKY7 (also known as SARKIa, SARKIaha), CDC2 (also known as CDKI), PRK), human cellular protein phosphatases such as FTP-SL (also known as MCPB3) and PTP-seta, the cellular signal transduction molecules HSPB0 and GPIR-1. The invention is useful for regulating the production of prions in cells and in the manufacture of pharmaceutical composition for prophylaxis and/or treatment of infectious disease (e.g. Scrapie, chronic wasting disease (CWD), transmissible mink encephalopathy (TWE), Creutzfeldt-Jacob disease (CWD), bovine spongiform encephalopathy (BSE), variant CJD, Gersmann-Straussler-Scheinker syndrome (GSS), fatal familial insomnia (FRI), Kuru and Alpers syndrome, especially BSE, CJD, vCJD) or neurodegenerative diseases (e.g., Alzheimer's disease) in humans or ruminants. The present sequence is human FGF-RI protein used in the

Gaps ö Length 822; 0; Indels ch 100.0%; Score 107; DB 6; 25; Conservative 0; Mismatches 0; 409 HSQMAVHKLAKSIPLRRQVIVS 430 1 HSQMAVHKLAKSIPLRRQVTVS 22 Query Match Best Local Similarity Matches 22; Conserv Sequence 822 AA; g

2, 2004, 09:29:31

completed: August ne : 14.8947 secs

Search cor Job time

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

2, 2004, 09:26:54; Search time 3.32895 Seconds (without alignments) 635.701 Million cell updates/sec August Run on:

US-09-757-415A-3 Title:

1 HSQMAVHKLAKSIPLRRQVTVS Perfect score: Sequence:

, Gapext Gapop 10.0 BLCSUM62 Scoring table:

283366 segs, 96191526 residues

Searched:

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 8 8 9 9 0 0 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

heparin-binding gr fibroblast growth fibroblast growth fibroblast growth fibroblast growth fibroblast growth fibroblast growth fibroblast growth fibroblast growth fibroblast growth fibroblast growth fibroblast growth fibroblast growth fibroblast growth fibroblast growth fibroblast growth fibroblast growth fibroblast growth fibroblast growth fibroblast growth keratinocyte growt fibroblast growth fibroblast growth fibroblast growth fibroblast growth fibroblast growth keratinocyte growt fibroblast growth fibroblast growth heparin-binding gr fibroblast growth protein-tyrosine k protein-tyrosine k growth ibroblast growth ibroblast growth fibroblast C40862 I49293 TVHUFG TVMSFG S29840 I49289 A39752 TVCHFG A56795 A38429 S16236 S17295 TVMSBK TVHUF2 A41794 B54846 A36477 I65223 A54846 B35963 S24108 S36439 S41050 A45081 DB Query Match Length 1000.00 1000.00 1000.00 1000.00 1000.00 88.88 87. Score Result No.

fibroblast growth	fibroblast growth	fibroblast growth	perlecan precursor	hypothetical prote	DNA-binding protei	heparan sulfate pr	fibroblast growth	AL2 protein - toma	transposase BMEI14	IS66 family Orf4 (ribosomal protein	phosphoglucomutase	fibroblast growth	fibroblast growth	hypothetical prote
A56182	B56182	A49123	A38096	T26135	835633	S18252	150128	QQCVC4	AI3429	AC3205	B97285	G82299	JC4058	838579	H95095
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62.6	62.6	62.6	43.9	43.	42.	42.	41.	40	40	40.	40.	40.	40.	39	39
67 62.6	7		47 43.9		45.5 42.	45 42.		43.5 40.			43 40.	43 40.	43 40.	42.5 39	~

ALIGNMENTS

C40862							
heparin-binding growth factor receptor variant alpha-a2	gu	growth	factor	receptor	variant	alpha-a2	mnų -
C; Species: Homo sapiens (man)	ě	sapiens	(man)				

RESULT 1

Cibate: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 16-Jul-1999
Cibate: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 16-Jul-1999
Cibates: Cassion: C40662
Cibate: 251, 665-668, 1991
A;Title: Fibitoblast growth factor receptors from liver vary in three structural domains.
A;Reterence number: A40862; MUID:91126480; PMID:1846977
A;Recession: C40862
A;Retus: preliminary
A;Recession: C40862
A;Retus: preliminary
A;Residues: 1-662 <HOJO
A;Cross-references: GB:MG1388
A;Residues: 1-662 <HOJO
A;Cross-references: GB:MG1388
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protes)
C;Reywords: ATP; growth factor receptor; heparin binding; transmembrane protein
F;171-232/Domain: immunoglobulin homology atMM>
F;377-399/Domain: transmembrane #status predicted <TWM>
F;377-399/Domain: protein kinase homology #status atypical <KIN>
F;484-492/Region: protein kinase ATP-binding motif

Gaps ö 100.0%; Score 107; DB 2; Length 662; 100.0%; Pred. No. 1e-09; ive 0; Mismatches 0; Indels o 100.0%; Pre Query Match Best Local Similarity 100. Matches 22; Conservative

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g ò

RESULT 2

fibroblast growth factor receptor-1, short isoform precursor - mouse c; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: 14223
R; Jin, Y: Pasumarthi, K.B.; Bock, M.B.; Lytras, A.; Kardami, E.; Cattini, P.A.
J. Mol. Cell. Cardiol. 26, 1449-1459, 1994
A; Title: Cioning and expression of fibroblast growth factor receptor-1 isoforms in the mc A; Reference number: 149289; MUID:95205422; PMID:7897669
A; Accession: 14223
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
C; Status: preliminary; translated from GB/EMBL/DDBJ
C; Status: preliminary; translated from GB/EMBL/DDBJ
C; Status: preliminary; translated from GB/EMBL/DDBJ
C; Superfamily: basic fibroblast growth factor receptor c; Keywords: ATP; growth factor receptor c; Reywords: ATP; Growth factor receptor c; Reference

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A;Status: not compared with conceptual translation
A;Status: not compared with conceptual translation
A;Residues: 71-132 <JO3>
A;Residues: 71-132 <JO3>
B;Ruta, M.; Howk, R.; Ricca, G.; Drohan, W.; Zabelshansky, M.; Laureys, G.; Barton, D.E.;
Chcogene 3; 9-15, 1988
A;Title: A novel protein tyrosine kinase gene whose expression is modulated during endot)
A;Reference number: A28361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: mRNA
A,Residues: 201-671, IYLTGS, 677-822 <RUT>
A,Residues: 201-671, IYLTGS, 677-822 <RUT>
A,GCOSS-Izeferences: EMBL:Y00665
R,Hattori, Y.; Odagiri, H.; Katoh, O.; Sakamoto, H.; Morita, T.; Shimotohno, K.; Tobinai,
Cancer Res. 52, 3367-3371, 1992
A,Title: K.Sam.-related gene, N-Sam, encodes fibroblast growth factor receptor and is exp:
A,Reference number: S25420; WUID:92282615; PMID:1317750
A,Accession: S25420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Molecule type: mRNA
;Residues: 1-30,120-822 <BI3>
;Cross-references: EMBL:X57119; NID:g31388; PIDN:CAA40401.1; PID:g31389
;Oross-reference from Fig. 3 is inconsistent with that from Fig. 1 in lacking 25-Pro;
;Note: this form is designated isoform II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Molecule type: mRNA
, Residues: 1-90, 'D', 91-822 <EL2>
, Cross-references: EMBL:X57121
, Note: the sequence from Fig. 3 is inconsistent with that from Fig. 1 in lacking 25-Pro;
, Note: this form is designated isoform III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Residues: 1-822 (HAT).
A, Rosidues: 1-82 (HAT).
A, Cross-references: EMBL: X66945, NID:935109, PIDN: CAA47375.1, PID:935110

R, Cross-references: EMBL: X66945, NID:935109, P. Dell'Era, P.; Zoppetti, G.; Oreste, P.; Valsasir Biochem: Biophys. Res. Commun. 203, 450-458, 1994

A, Title: Distinct role of 2-O-, N-, and 6-O-sulfate groups of heparin in the formation of A, Reference number: PC2394; MUID:94354840; PMID:8074689
Title: Alternative splicing generates at least five different isoforms of the human bas. Reference number: S17373, MUID:91319400; PMID:1650441
                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-30,120-147,150-822 <EI4>
A;Cross-references: EMBL:X57122; NID:g31386; PIDN:CAA40404.1; PID:g31387
A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 1 in lacking 25-Pro
A;Note: this form is designated isoform I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-90, 'D', 91-147,150-822 <EIS>
A; Cross-references: EMBL: K57120
A; Cross-references: EMBL: K57120
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A; Mr. Sebert Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Septemble Se
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A; Residues: 1-30,120-147,150-468, 'L',470-822 < ITO>
A; Cross-references: GB:M37722; NID:g179413; PIDN:AAA75007.1; PID:g179415
A; Note: both the longer and shorter forms are expressed in the placenta
B; Johnson, D.E.; Lee, P.L.; Lu, J.; Milliams, L.T.
Mol. Cell. Biol. 10, 4728-4736; 1990
A; Fitle: Diverse forms of a receptor for acidic and basic fibroblast growth factors.
A; Reference number: A36464; MUID:90355989; PMID:2167437
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;Residues: 1-30,120-147,150-191,'E',193-822 <JO2>
;Cross-references: GB:M34186; NID:g182533; PIDN:AAA35837.1; PID:g182534
;Accession: B36464
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;Residues: 1-30,120-822 <JOH>
;Cross-references: GB:M34185; NID:g182531; PIDN:AAA35836.1; PID:g182532
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A,Molecule type: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fibroblast growth factor receptor 1 precursor - human
NyAlternate names: basic fibroblast growth factor receptor; heparin-binding growth factor
NyAlternate names: basic fibroblast growth factor receptor; heparin-binding growth factor
NyContains: HBGFR 3; HBGFR alpha b1; HBGFR beta a1; HBGFR beta b1; HBGFR gamma a1; HBGFR
NyContains: HBGFR 3; HBGFR alpha b1; HBGFR beta a1; HBGFR gamma a1; HBGFR
NyContains: HBGFR 3; HBGFR alpha b1; HBGFR beta a1; HBGFR gamma a1; HBGFR
NyContains: S1082; Bacquence revision 31-Dec-1993 #text change 16-Jul-1999
NyContains: S1082; Bacquence revision 31-Dec-1993 #text change 16-Jul-1999
NyContains: S1082; Ballot, F.; Kaplow, J.M.; Searfoss, G.; Ruta, M.; Burgess, AyFitler: Cloning and expression of two distinct high-affinity receptors cross-reacting w
AyRocession: S11692.
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A;Cross-references: EMBL:X51803; NID:g31367; PIDN:CAA36101.1; PID:g31368
R;Wennstroem, S.; Sandstroem, C.; Claesson-Welsh, L.
Growth Factors 4, 197-208, 1991
A;Title: CDNA cloning and expression of a human FGF receptor which binds acidic and basi A;Reference number: A61533; MUID:92118394; PMID:1722683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Cross-references: EMBL:X52833; NID:g31377; PIDN:CAA37015.1; PID:g31378
R;Hou, J.; Kan, M.; McKeehan, K.; McBride, G.; Adams, P.; McKeehan, W.L.
Science 251, 665-668, 1991
A;Title: Fibroblast growth factor receptors from liver vary in three structural domains.
A;Reference number: A40862; MUID:91126480; PMID:1846977
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A; Residues: 1-147,150-193,'S',195-822 < WEN>
A; Residues: 1-147,150-193,'S',195-822 < WEN>
A; Cross-references: GB:M34641; NID:9182529; PIDN:AAA35835.1; PID:9182530
A; Experimental source: teracarcinoma cell line Tera-2
R; Kiefer, M.C.; Baird, A.; Nguyen, T.; George-Nascimento, C.G.; Mason, O.B.; Boley, L.J.
Growth Reacors S, 115-127, 1991
A; Title: Molecular cloning of a human basic fibroblast growth factor receptor cDNA and e
A; Reference number: A61536; MUID:92118399; PMID:1662973
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A, Residues: 1-822 < HOUS
A, Residues: 1-822 < HOUS
A, Cross-references: GB: M63887
A, Note: potentially twelve variants may arise by alternative splicing in liver cells
R, Isacchi, A.; Bergonzoni, L.; Sarmientos, P.
Nucleic, Acids Res. 18, 1906, 1990
Nucleic, Complete sequence of a human receptor for acidic and basic fibroblast growth A, Reference number: S09226; MUID: 90245600; PMID: 2159626
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A;Cross-references: EMBL:X57120; NID:g31390; PIDN:CAA40402.1; PID:g31391
R;Elsemann, A.; Ahn, J.A.; Graziani, G.; Tronick, S.R.; Ron, D.
Oncogene 6, 1195-1202, 1991
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A,Accession: S26738
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          100.0%; Score 107; DB 2;
100.0%; Pred. No. 1.1e-09;
ive 0; Mismatches 0;
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R;Tronick, S.R.
Submitted to the EMBL Data Library, January 1991
A;Reference number: 819167
A;Accession: 826739
                                                                                                                                                                                                                                                                                                             320 HSQMAVHKLAKSIPLRRQVTVS 341
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                                                            ilarity 100.0%;
Conservative (
                                                                 Similarity
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A, Residues: 1-822 <DIO>
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A, Molecule type: mR
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          Query Match
Best Local S
Matches 22
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A;Reference number: A35794; MUID:90272715; PMID:2161540
A;Accession: A35794
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1.30,120-228,'S',230-255,'ILQ',259-269,'A',271-543,'M',545-628,'LV',631-755,'A;Residues: 1.30,120-228,'S',230-255,'ILQ',259-269,'A',271-543,'M',545-628,'LV',631-755,'A;Reference number: A43025
A;Reference number: A43025
A;Reference number: A43025
A;Reference number: A43025
A;Residues: 1.30,120-228,'S',230-255,'ILQ',259-269,'A',271-543,'M',545-755,'R',757-764,'IRA esidues: 1.30,120-228,'S',230-255,'R',137-163,'IS94
A;Title: Murine fibroblast growth factor receptor 1 gene generates multiple messenger RNF
A;Reference number: PC2277; MUID:99100926; PMID:7802632
A;Accession: PC2277; MUID:99100926; PMID:7802632
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F)398-822/Domain: protein Kinase homology <XIN>
F)484-492/Domain: protein Kinase homology <XIN>
F)484-492/Region: protein Kinase ATP-binding motif
F)55-101,170-230,277-341/Disulfide bonds: #status predicted
F)571.117,227,240,264,396,317,330/Binding site: carbohydrate (Asn) (covalent) #status predicted
F)514,531,623/Active site: Lys, Glu, Asp #status predicted
F)528,641/Binding site: magnesium (Asn, Asp) #status predicted
F)54/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted
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C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protes
C;Keywords: ATP; autrophosphorylation; growth factor receptor; phosphoprotein; transmembre
F;171-232,Domain: immunoglobulin homology <INN>
F;476-761/Domain: protein kinase homology <INN>
F;484-492/Region: protein kinase ATP-binding motif
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A; Molecule type: DNA
A; Molecule 1-15 cHAA.
A; Cross-references: GB: S74765; NID: 9833887; PIDN: AAB32845.1; PID: 9833889
C; Comment: This protein mediates the biological actions of heparin-binding growth factors
C; Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protein
C; Reywords: alternative splicing; ATP; autophosphorylation; duplication; glycoprotein; gn
protein kinase
F;1-21/Domain: signal sequence #status predicted <SIG>
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CiSpecies: Rattus norregicus (Norway rat)
CiSpecies: Rattus norregicus (Norway rat)
CiSpecies: Rattus norregicus (Norway rat)
CiSpate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
CiAccession: S29840
R; Yazaki, N.; Fujita, H.; Ohta, M.; Kawasaki, T.; Itoh, N.
Biochim: Biophys. Acta 1172, 37-42, 1993
A; Ritle: The structure and expression of the FGF receptor-1 mRNA isoforms ir
A; Reference number: S29840; MUID:93176824; PMID:8382532
A; Satus: preliminary
A; Moleçule type: mRNA
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Pred. No. 1.3e-09;
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Pred. No. 1.3e-09;
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NyAlternate names: basic fibroblast growth factor receptor
NyAlternate names: basic fibroblast growth factor receptor
NyAlternate names: basic fibroblast growth factor receptor
NyAlternate names: basic fibroblast growth factor receptor
Cypecies: Nus musculus (house mouse)
Cypecies: Nus musculus (house mouse)
Cypecies: Nus musculus (house mouse)
Cypecies: Nus musculus (house mouse)
NyAccession: A38849; Barnard
Oyaccession: A38849; MUID:90160373; PMID:1689490
AyTitle: Two forms of the basic fibroblast growth factor receptor-like mRNA are expresse
AyCross-references: GBN28998; NID:90160373; PMID:1689490
AyMolecule type: mRNA
AyCross-references: GBN28998; NID:9192164; PIDN:AA37290.1; PID:g309116
AyCross-references: GBN28998; NID:9192164; PIDN:AA37290.1; PID:g309116
AyCross-references: GBN28998; NID:g192164; PIDN:AA37290.1; PID:g309116
AyCross-references: GBN28999; NID:g192164; PIDN:AA37290.1; PID:g109116
AyCross-references: GBN28999; NID:90265603; PMID:2161096
AyTitle: The murine fig gene encodes a receptor for fibroblast growth factor.
AyReference number: 809993; NUID:90265603; PMID:2161096
AyTitle: The murine fig gene encodes a receptor for fibroblast growth factor.
AyReference number: 809993; NID:90265603; PMID:2161096
AyResidues: 1-147.160-225, TIQ', 259-439; A'A', 441-755, A'A', 757-822 cSAF>
AyCross-references: BBBL:X51893; NID:g50959; PIDM:CA336175.1; PID:550960
ByCross-references: BBBL:X51893; NID:34-4384, 1990
AyTitle: A murine fibroblast growth factor (FGF) receptor expressed in CHO cells is actil
                                  A; Residues: 81-100 < RUS>
A; Residues: 81-100 < RUS>
A; Exeriduets la source: recombinant soluble form of extracellular domain after expression A; Experimental source: recombinant soluble form of a 33K fragment protected from trypsin C; Comment: This receptor binds acidic and basic fibroblast growth factors with high affice Generics: Generics: Spin 119913; OMIN:136350
A; Cross-references: GBB:119913; OMIN:136350
A; Cross-references: GBB:119913; OMIN:136350
A; Cross-references: GBB:119913; OMIN:136350
A; Cross-references: GBB:119913; OMIN:136350
A; Map position: Bpl1.2-8pl1.1
C; Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote C; Keywords: alternative splicing; ATP; autophosphorylation; duplication; glycoprotein; G; Stywords: alternative splicing; ATP; autophosphorylation; form alpha al #status predicted F; G; Stywords: alternative growth factor receptor 1, form alpha bl #status predicted F; Gz-47, 430-822/Product: fibroblast growth factor receptor 1, form beta all #status predicted F; Gz-30, 120-422/Product: fibroblast growth factor receptor 1, form gamma bl #status predicted F; Grown and F; Grown and F; Grown and F; Grown and F; Grown and F; Grown and F; Grown and F; Grown and F; Grown and F; Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and Grown and 
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100.0%; Pred. No. 1.3e-09;
ive 0; Mismatches 0;
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C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protei C;Keywords: alternative splicing; ATP; autophosphorylation; duplication; glycoprotein; grotein kinase
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F;22-814/Product: fibroblast growth factor receptor A1, long splice form #status experime
F;22-372/Domain: extracellular #status predicted <EXT>
F;22-30,119-814/Product: fibroblast growth factor receptor A1, short splice form #status
F;77-102/Domain: immunoglobulin homology <IM1>
                                                                                                                                                                                                                                         protein-tyrosine kir
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Nyllernate names: basic fibroblast growth factor receptor
Nyllernate names: basic fibroblast growth factor receptor
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 31.Dec.1993 #text_change 16-Jul-1999
C;Accession: A41345; A33908
R;Lee, P.L.; Johnson, D.E.; Cousens, L.S.; Fried, V.A.; Williams, L.T.
Science 245, 77-60, 1989
A;Title: Purification and complementary DNA cloning of a receptor for basic fibroblast A;Reference number: A41345; WID:89298406; PMID:2544996
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A Astaus: nucleic acid sequence not shown; not compared with conceptual translation
A, Molecule type: mRNA
A, Residues: 1-819 - LLEE>
A, Note: part of the sequence was confirmed by protein sequencing
                                                                                                                                                                                                                                                                             Cispecies: Xenopus laevis (African clawed frog)
Cibate: 07-Feb-1992 Hasquence_revision 19-Jan-1996 #text_change 16-Jul-1999
Cipacession: A39752; B39752
Ririesel, R.; Dawid, I.B.
Mol. Cell. Biol. 11, 2481-2488, 1991
A;Tille: cDNA cloning and developmental expression of fibroblast growth factor A;Reference number: A39752; MUDI:91203867; PMID:1850097
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fibroblast growth factor receptor Al precursor - African clawed frog
N;Contains: fibroblast growth factor receptor Al, short splice form;
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Proc. Natl. Acad. Sci. U.S.A. 86, 5449-5453, 1989

A;Title: Identification of a developmentally regulated pa;Reference number: A33908; MUD:89315814; PMID:2473471

A;Molecule type: mRNA
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Best Local Similarity
Matches 20; Conserv
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C;Species: Mus musculus (house mouse)
C;Dacession: 14928
C;Dacession: 149289
R;Jin, Y.; Pasumarthi, K.B.; Bock, M.E.; Lytras, A.; Kardami, B.; Cattini, P.A.
J. Mol. Cell. Cardiol. 26, 1449-1459, 1994
R;Jin, Y.; Pasumarthi, K.B.; Bock, M.E.; Lytras, A.; Kardami, B.; Cattini, P.A.
J. Mol. Cell. Cardiol. 26, 1449-1459, 1994
A;Title: Cloning and expression of fibroblast growth factor receptor-1 isoforms in the M;Reference number: 149289; MUID:95205422; PMID:7897669
A;Reference number: 149289
A;Reference number: 149289
A;Reference number: 149289
A;Cattas: preliminary; translated from GB/EMBL/DDBJ
A;References: EMES.
A;Cross-references: EMES.
A;Cross
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A/Festures: 1-823 c.KNUD.
A/Festures: 1-823 c.KNUD.
A/Festures: 1-823 c.KNUD.
A/Festures: 1-824.6. English (1993292; PIDN:AAA37620.1; PID:g193293
A/Festures: 1-824.6. English (1992)
A/Festures: 1-82-832 c.KNUD.
A/Festures: 1-82-832 c.KNUD.
B/Festures:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bre
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R;Koubara, H.; Kasayama, S.; Saito, H.; Matsumoto, K.; Sato, B.
Biochem. Biophys. Res. Commun. 176, 31-37, 1991
A,Title: Expression CDNA cloning of fibroblast growth factor (FGF) receptor in mouse lA;Reference number: JH0393; MUID:91207411; PMID:1708247
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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
           Gaps
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100.0%; Pred. No. 1.3e-09;
tive 0; Mismatches 0;
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Pred. No. 1.3e-09;
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     Mismatches
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Matches 22; Conservative
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A; Residues: 1-832 <KOU>
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A, Reference number: A36477; MUID:91045998; PMID:2172985
A, Accession: A34477
A, Accession: A34477
A, Molecule type: mRNA
A, Residues: 1.812 cMUS
A, Accession: A34474
A, Residues: L. 812 cMUS
A, Accession: A3472 developmental capters of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the problem of the probl
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Residues: 1-415 cRES>
A,Cross-references: GB:L19106; NID:g310144; PIDN:AAB02867.1; PID:g310145
A,Accession: 165226
A,Accession: 165226
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Roloule type: mRNA
A,Residues: 1-415 cRED>
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R;Yan, G.; McEride, G.; McKeehan, W.L.
Biochem. Biophys. Res. Commun. 194, 512-518, 1993
A;Title: Exon skipping causes alteration of the COCH-terminus and deletion of the phosphc
A;Reference number: I52281; MUID:93326167; PMID:8333865
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C,Species: Rattus norvegicus (Norway rat)
C,Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jul-2000
C,Accession: 165223; 165226
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86.4%; Pred. No. 1.8e-07;
ive 3; Mismatches 0; Indels
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llarity 85.7%; Pred. No. 6.4e-06;
Conservative 0; Mismatches 3;
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                                                                                      A;Cross-references: (BE:M24637
A;Fote: this protein is expressed in embryonic tissues and, at low levels, in adult brain [C;Genetics:
A;Gene: cek.
C;Genetics:
A;Gene: cek.
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote [C;Reywords: ATP; autophosphorylyrid adult at all all advantages and factor receptor 1; immunoglobulin homology; prote [C;Reywords: ATP; autophosphorylyrid adult at a growth factor receptor 1 #status predicted <MAT>
F;22-819/Product: fibroblast growth factor receptor 1 #status predicted <MAT>
F;22-819/Product: fibroblast growth factor receptor 1 #status predicted <MAT>
F;169-230/Domain: extracellular #status predicted <TMM>
F;350-839/Domain: inmunoglobulin homology <IMM>
F;350-839/Domain: intracellular #status predicted <IMT>
F;350-839/Domain: intracellular #status predicted <IMT>
F;4474-759/Domain: protein kinase homology <KIN>
F;482-490/Region: protein kinase homology <KIN>
F;482-400/176-228,275-339/Disulfide bonds: #status predicted F;65,116,225,238,265,294,315,338/Binding site: carbohydrate (Asn) (covalent) #status predicted F;651,165,25,238,265,294,315,338/Binding site: magnesium (Asn, Asp) #status predicted F;625,639/Binding site: magnesium (Asn,
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A36477

Nibroblast growth factor receptor A2 precursor - African clawed frog

Nicontains: fibroblast growth factor receptor A2, short splice form; protein-tyrosine ki

C;Species: Xenopus laevis (African clawed frog)

C;Abecies: OB-Mar-1991 #sequence_revision 19-Jan-1996 #text_change 16-Jul-1999

C;Accession: A36477; C39752

R;Musci, T.J.; Amaya, E.; Kirschner, M.W.

Proc. Natl. Acad. Sci. U.S.A. 87, 8365-8369, 1990

A;Title: Regulation of the fibroblast growth factor receptor in early Xenopus embryos.
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A/Molecule type: mRNA
A/Molecule type: mRNA
A/Molecule type: mRNA
A/Molecule type: mRNA
A/Molecule type: mRNA
A/Molecule type: mRNA
A/Molecule type: mRNA
A/Cross-references: (BB:854008; NID:9264804; PIDN:AAB54274.1; PID:9264805
A/Note: sequence extracted from NCBI backbone (NCBIN:124259; NCBIP:124270)
C/Superfamily: basic fibrobiast growth factor receptor 1; immunoglobulin homology; prote
C/Superfamily: basic fibrobiast growth factor receptor
F#80-141/Domain: immunoglobulin homology < MINA
F#383-668/Domain: protein kinase homology < MINA
F#391-399/Region: protein kinase AIP-binding motif
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                                           A;Residues: 1-89,'A',91-685,'M',687-819 <PAS>
A;Cross-references: GB:M24637
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nes 19; Conservative
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412 SÓPAVHKLTKRIPLRRÓVTVS 432
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ne : 4.32895 secs
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B. Takagi, Y.; Shivastav, S.; Miki, T.; Sakaguchi, K.

B. Takagi, Y.; Shivastav, S.; Miki, T.; Sakaguchi, K.

J. Biol. Chem. 259, 23143.23149, 1994

A. Title: Molecular cloning and expression of the acidic fibroblast growth factor receptor lilty and covalent attachment of heparan sulfate glycosaminoglycan to the receptors: Asefetence number: A54846; MUID: 94375484; PMID: 8089146

A. Accession: A54846

A. Accession: A54846; MUID: 94375484; PMID: 8089146

A. Accession: A54846

A. Accession: Compared with conceptual translation

A. Residues: 1-707 < TAX>
C. Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote fixeywords: ATP; growth factor receptor 1; immunoglobulin homology < IMM>
F. 57-118/Domain: immunoglobulin homology < IMM>
F. 365-650/Domain: protein kinase homology < KIN>
F. 373-381/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        keratinocyte growth factor receptor precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 16-Jul-1999
C;Accession: A38429
R;Miki, T.; Fleming, T.P.; Bottaro, D.P.; Rubin, J.S.; Ron, D.; Aaronson, S.A.
Science 251, 72-75, 1991
A;Fitle: Expression cDNA cloning of the KGF receptor by creation of a transforming autoc
A;Feference number: A38429; MUID:91095977; PMID:1846048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: GE:M63503, NID:g198593, PIDN:AAA39377.1; PID:g198594
C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
C;Superfamily: artophosphorylation; growth factor receptor; phosphoprotein; transmembz
F;57-118/Domain: immunoglobulin homology <IMM>
F;365-650/Domain: protein kinase homology <IMN>
F;365-650/Domain: protein kinase homology <IMN>
F;373-381/Region: protein kinase ATP-binding motif
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0
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Species: Homo sapiens (man)
C,Date: 16-Sep.1992 #sequence_revision 16-Sep-1992 #text_change 16-Jul-1999
C,Accession: S16236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
77.6%; Score 83; DB 2; Length 707
Best Local Similarity 85.7%; Pred. No. 1.1e-05;
Matches 18; Conservative 0; Mismatches 3; Indels
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                                           SOPAVHKLTKRIPLRROVTVS 25
   SOMAVHKLAKSIPLRROVTVS 22
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A;Molecule type: mRNA
A;Residues: 1-707 <MIX>
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A.Molecule type: mRNA
A.Residues: 1-769 <ERNA
A.Fesidues: 1-769 <ERNA
A.Cross-references: EMBL.X56191, NID:929431, PIDN:CAA39654.1; PID:929432
C.Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; protei
C.Superfamily: basic fibroblast growth factor receptor; glycoprotein; growth factor receptor;
F.1-21/Domain: signal sequence #status predicted <SIG>
F.22-769/Product: fibroblast growth factor receptor #status predicted <MAT>
F.22-378/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fi132-1337)Comain: actual actual actual predicted <TMM>
Fi172-233/Domain: immunoglobulin homology <IPMN>
Fi379-399/Domain: transmembrane #status predicted <TMM>
Fi300-369/Domain: intracellular #status predicted <INT>
Fi480-765/Domain: protein kinase homology <KIRN>
Fi488-496/Region: protein kinase APP-binding motif
Fi213-2131,278-340/Disulfide bonds: #status predicted
Fi33.123,228,241,265,297,318,329,356/Binding site: carbohydrate (Asn) (covalent) #status
Fi518,535,627/Active site: Lys, Glu, Asp #status predicted
R;Seno, M.; Sasada, R.; Watanabe, T.; Ishimaru, K.; Igarashi, Biochim. Biophys. Acta 1089, 244.246, 1991
A;Title: Two cDNAs encoding novel human FGF receptor.
A;Reference number: S16236; WUID:91274356; PMID:1647213
A;Accession: S16236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;132-138/Region: acidic
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Gaps . 0

77.6%; Score 83; DB 2; Length 769 85.7%; Pred. No. 1.2e-05; .ive 0; Mismatches 3; Indels

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2, 2004, 09:31:50

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: August 2, 2004, 09:23:08; Search time 2.31579 Seconds
(without alignments)
494.666 Million cell updates/sec

US-09-757-4158-3

Title: US-09-757-415A-3
Perfect score: 107
Sequence: 1 HSQMAVHKLAKSIPLRRQVTVS 22

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Total number of hits satisfying chosen parameters: 141681

141681 seqs, 52070155 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

דומנדות דודמני דר מכי

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	HUMAN P11362 homo sapien	mus muscu	Q04589 rattus	gallus g	P22182 xenop	P21802 homo sap	2 P21803 mus m	P18461 gallus g	. Q03364 xenor	P98160 home	P40694 mus n	Q05793	P27262	Q81fg2	Q9nzn4	Q10887 myco	095503 hom	mus m	P45724 ara	036164	P15541 oryctolagu	P22607	099090	bacillu	chlam	P17600	P17599 b	ASPNG 042804 aspergillus	ч	mus mu	P57075	drogo
500		FGR1 HU	FGR1 MO	FGR1_RAT	FGR1 CH					FGR2_XE	PGBM_HUMAN	SMB2_MO	PGBM MOUSE	VAL2_TYLCV	AROB BACCR	EHD2 HUMAN	X090 MY	CBX6_HU	CBX6 MO	PAL2_AR			FGR3 HU	SMB2 ME				SYN1_BO		ABL1 HU	FGR3 MO	UAS3 HU	VEMA DR
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Q9vm75 drosophila	Q44697 buchnera ap	_	Q8xbj4 escherichia			P33995 escherichia	Q8z3g1 salmonella	Q8zlr8 salmonella	P17163 klebsiella	Q9za87 proteus mir	08zb41 yersinia pe
BP28 DROME	TRPE BUCDN	TRBD RHISN	UCPA_ECO57	UCPA SALTY	TC1A CAEEL	YHBJ_ECOLI	YHBJ SALTI	YHBJ SALTY	YPTO_KLEOX	YPTO PROMI	YZ86_YERPE
г	Н	Н	-1	H	Н		_	Н	_	Н	Н
2096	519	66	263	263	273	284	284	284	284	284	284
36.4	36.0	35.5	35.5	35.5	35.5	35.5	35.5	35.5	35.5	35.5	35.5
9	38.5	38	38	38	38	38	38	38	38	38	38
34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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	RAPARARARARARARARARARARARARARARARARARAR	요요

Nature 358:678-681(1992).

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MEDLINE-2238257; Pubmed-12477932;

X TISSUE-Therus,

X Strausberg R.L., Feingold E.A., Grouse I.H., Derge J.G.,

X Altschul S.F., Zeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Zeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

X Brans S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

X Richards S., McKwan P.J., McKernan K.J., Malek J.A., Gunzathe P.H.,

X Richards S., Worley K.C., Hale S., Garcia A.M., Galbs R.A.,

X Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

X Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

X Hakesley R.W., Maray D.W., Sodergren E.J., Lu X., Gibbs R.A.,

X Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

X Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

X Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

X Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

X Cheerzation and initial analysis of more than 15,000 full-length
                                                                              TISSUE=Placenta;
MEDLINE=90290512; PubMed=2162671;
IIOh N., Terachi T., Ohta M., Seo M.K.;
"The complete amino acid sequence of the shorter form of human basic fibroblast growth factor receptor deduced from its CDNA.";
Biochem. Biophys. Res. Commun. 169:680-685(1990).
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 201-822 FROM N.A.

Ruta M., Howk R., Ricca G., Drohan W., Zabelshansky M., Laureys G.,
Barton D.B., Francke U., Schlessinger J., Givol D.;
"A novel protein tyrosine kinase gene whose expression is modulated
during endothelial cell differentiation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINES-20355989; PubMed=216/4137,
Johnson D.E., Lee P.L., Lu d., Williams L.T.;
"Diverse forms of a receptor for acidic and basic fibroblast growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91319400, PubMed=1650441;
Eisemann A., Ahn J.A., Graziani G., Tronick S.R., Ron D.;
"Alternative splicing generates at least five different isoforms of
the human basic-FGF receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91141499; PubMed=1847500;
Gutkind S.J., Link D.C., Katamine S., Lacal P., Miki T., Ley T.J.,
Robbins K.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDINE=92357144; PubMed=1379697;
Peters K.G., Marie J., Wilson E., Ives H.E., Escobedo J.,
Peters K.G., Marie J., Williams L.T.,
Polit mutation of an FGF receptor abolishes phosphatidylinositol
turnover and Ca2+ flux but not mitogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A novel c-fgr exon utilized in Epstein-Barr virus-infected B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wennstroem S., Sandstroem C., Claesson-Welsh L.;
Submitted (JUL-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell. Biol. 10:4728-4736(1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTERNATIVE SPLICING
[6]
SEQUENCE FROM N.A.
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-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
-!- DATABASE: NAMS=Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW="http://www.infobiogen.fr/services/chromcancer/Genes/FGFR1113.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the FWBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isold=P11362-7; Sequence=VSP_002959;
DISBASE: Defects in FGFR1 are one of the causes of Pfeiffer syndrome (PS) [MIM:101600]; also known as acrocephalosyndactyly type V (ACSS). PS is characterized by craniosynostosis (premature fusion of the skull sutures) with deviation and enlargement of the numbs and great toes, brachymesophalangy, with phalangeal ankylosis and a varying degree of soft tissue syndactyly. DISBASE: Involved in a t (8:13) (p12:q12) chromosomal translocation which involves FGFR1 and ZNF199: The resulting transcript is a possible candidate for seem cell leukemia lymphoma syndrome/SCLi. SIMILARITY: Belongs to the fibroblast growth factor receptor
                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 464-762.
MEDLINE=96361355; PubMed=8752212;
Mohammadi M., Schlessinger J., Hubbard S.R.;
"Structure of the FGF receptor tyrosine kinase domain reveals a novel autoinhibitory mechanism.";
Cell 86:577-587(1996).
                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 464-762.

MEDILINE=7784786; PubMed=9139660;

Mohammadi M., McMahon G., Sun L., Tang C., Hirth P., Yeh B.K.,

Hubbard S.R., Schlessinger J.;

"Structures of the tyrosine kinase domain of fibroblast growth factor
receptor in complex with inhibitors.";

Science 276:955-960(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95179173; PubMed-7874169; Muenke M., Schill U., Hehr A., Robin N.H., Losken H.W., Schill D., Hehr A., Robin W., Malcolm S., Winter R.M.; Pulleyn L.J., Rutland P., Reardon W., Malcolm S., Winter R.M.; Pommon mutation in the fibroblast growth factor receptor 1 gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- FUNCTION: Receptor for basic fibroblast growth factor. A shorter form of the receptor could be a receptor for acidic FGF (aFGF).
-i- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                          Mohammadi M., Dionne C.A., Li W., Lin N., Spivak T., Honegger A.M., Jaye M., Schlessinger J.;
                                                                                                                  "Point mutation in FGF receptor eliminates phosphatidylinositol hydrolysis without affecting mitogenesis."; Nature 158:681-684 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name-Beta B1;
IsoId=P11362-4; Sequence=VSP_002958, VSP_002960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing, Named isoforms=7;
Comment=Additional isoforms seem to exist;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P11362-5; Sequence=VSP_002957;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Alpha Al;
IsoId=Pll362-1; Sequence=Displayed;
                                      MUTAGENESIS OF TYR-766.
MEDLINE=92357145; PubMed=1379698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfeiffer syndrome.";
Nat. Genet. 8:269-274(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT PS ARG-252
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IsoId=P16092-1; Sequence=Displayed;

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splicing.";
Biochie. Blochys. Res. Commun. 205:1057-1063 (1994).
-!- FUNCTION: Receptor for basic fibroblast growth factor. A shorter form of the receptor could be a receptor for acidic FGF (aFGF).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=90272715; PubMed=2161540;
Mansukhani A., Moscatelli D., Talarico D., Levytska V., Basilico C.;
"A murine fibroblast growth factor (FGF) receptor expressed in CHO
cells is activated by basic FGF and Kaposi FGF.";
Proc. Natl. Acad. Sci. U.S.A. 87:4378-4382(1990).
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
MEDLINE=90160373; PubMed=1689490;
Reid H.H., Wilks A.F., Bernard O.;
"Two forms of the basic fibroblast growth factor receptor-like mRNA are expressed in the developing mouse brain.";
Proc. Natl. Acad. Sci. U.S.A. 87:1596-1600(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kouhara H., Kassyama S., Saito H., Matsumoto K., Sato B., "Expression cDNA cloning of fibroblast growth factor (FGF) receptor in mouse breast cancer cells: a variant form in FGF-responsive Eransformed cells.";

Biochem. Biophys. Res. Commun. 176:31-37(1991).
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MEDLINE=95100926; PubMed=7802632;
Harada T., Saito H., Kouhara H., Kurebayashi S., Kasayama S.,
Terakawa N., Kishimoto T., Sato B.,
"Murine fibroblast growth factor receptor 1 gene generates multiple
messenger RNAs containing two open reading frames via alternative
                                                                                                                                                                                                 FGR1 MOUSE STANDARD, FRT; 822 AA.
P16092; Q01736; Q61562;
P16092; Q01736; Q61562;
D1-ARR-1990 (Rel. 14, Created)
D1-MAY-1991 (Rel. 18, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Basic fibroblast growth factor receptor 1 precursor (EC 2.7.1.112)
FGFR1 OR FLG.
                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                      ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BALS/C; TISSUB=Brain; MEDLINE=9026563; PubMed=2161096; Safran A., Avivi A., Orr-Urtereger A., Neufeld G., Lonai P., Safran A., Yarden Y.; The murine flg gene encodes a receptor for fibroblast growth
    Length 822;
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
EVent-Alternative splicing; Named isoforms=3;
Name=1.
100.0%; Score 107; DB 1;
ilarity 100.0%; Pred. No. 2.1e-10;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING. MEDLINE=91207411; PubMed=1708247;
                                                                                                409 HSQMAVHKLAKSIPLRRQVTVS 430
                                                                            1 HSQMAVHKLAKSIPLRRQVTVS 22
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                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                    Local Similarity
es 22; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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      Query Match
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                        Best Loca
Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
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R PFINTS; PR00109; TYRKINASE.

R PRINTS; PR00109; TYRKINASE.

R PARDON; PR00109; TYRKINASE.

R SMART; SM00219; TYRKC; 1.

R SMART; SM00219; TYRC; 1.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE DOM; 1.

R PROSITE; PS00109; PROTEIN KINASE DOM; 1.

R PROSITE; PS00109; PROTEIN KINASE DOM; 1.

R PROSITE; PS00109; PROTEIN KINASE DOM; 1.

R PROSITE; PS00109; PROTEIN KINASE DOM; 1.

R PROSITE; PS00109; PROTEIN KINASE TYR; 1.

R PROSITE; PS00109; PROTEIN KINASE TYR; 1.

R PROSITE; PS00109; PROTEIN KINASE TYR; 1.

R PROSITE; PS00109; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE ATP; 1.

R PROSITE; PS00109; PROTEIN KINASE ATP; 1.
                                                 IsoId=Pi6092-3; Sequence=VSP 002961, VSP 002963;
SIMILARITY: Belongs to the fibroblast growth factor receptor
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                        -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                     PIRSP; A44849; TVMSFG.
HSSP; PI1362; IFGK.
MGD; MGI:95522; FgfrI.
GO; GO:0004202; FgfrI.
GO; GO:000435; P:inner ear morphogenesis; IMP.
GO; GO:0007435; P:salivary gland morphogenesis; IMP.
InterPro; IPR00710; Ig-like.
InterPro; IPR001719; Prof. kinase.
InterPro; IPR001455; Tyr_bkinase.
InterPro; IPR001455; Tyr_bkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 3.

APP (BY SIMILARITY).

ATP (BY SIMILARITY).
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                                      Synonyms=Variant;
                                                                                                                                                                                                                    EMBL, M28998, AAA37290.1; -.
EMBL, X51893, CAA36175.1; -.
EMBL, M65053, AAA37620.1; -.
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IsoId=P16092-2;
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                                      Name=3;
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VARSPLIC
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31

VARSPLIC

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Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                               BASIC FIBROBLAST GROWTH FACTOR RECEPTOR
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01-MAY-1991 (Rel. 18, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Basic fibroblast growth factor receptor 1 precursor (EC 2.7.1.112)
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MEDLINE=89315814; PubMed=2473471;
Pasquale E.B., Singer S.J.;
"Identification of a developmentally regulated protein-tyrosine kinase by using anti-phosphotyrosine antibodies to screen a cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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Prodom; PD000001; Prot_Kinase; 1.
SMART; SM00408; IGc2; 3.
SMART; SM00219; TyrKo; 1.
SMART; SM00219; TyrKo; 1.
PROSTE; PS50017; PROTEIN KINASE ATP; 1.
PROSITE; PS50010; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYP; 1.
TRANSFERSE; PS0POTCHIN; Tyrosine-protein kinase; ATP-binding; Transferase; Phosphorylation; Transmembrane; Signal; Immunoglobulin, domain; Repeat
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                                                                                                                                                                                                                                                                                                                                 CYTOPIASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY).
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Proc. Natl. Acad. Sci. U.S.A. 86:5449-5453(1989)
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N-LINKED ((N-LINKED (N-LINKED                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
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Best Local Similarity 100.0
Matches 22; Conservative
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822 AA;
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NCBI_TaxID=9031;
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P21804;
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Pasquale E.B.; Submitted (MAY-1989) to the EMBL/GenBank/DDBJ databases. [3]

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR007110; Ig-like.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR000719; Prot kinase.

R InterPro; IPR001245; Prot kinase.

R InterPro; IPR001245; Prot kinase.

R InterPro; IPR001245; Prot kinase.

R InterPro; IPR001245; Prot kinase.

R InterPro; IPR001245; Prot kinase.

R InterPro; IPR00104; Prot kinase.

R ProDom; Pr00006; Pkinase; 1.

R PR00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109; Pr00109
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PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
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BASIC FIBROBLAST GROWTH FACTOR RECEPTOR
SEQUENCE FROM N.A. MEDLINE=89298406; PEDLINE=89298406; PubMed=2544996; Lee P.L., Johnson D.E., Cousens L.S., Fried V.A., Williams L.T.; "Purification and complementary DNA cloning of a receptor for basic
                                                                                                                    fibroblast growth factor.";
Science 245:57-60(1989).
-!- FUNCTION: RECEPTOR FOR BASIC FIBROBLAST GROWTH FACTOR.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Belongs to the fibroblast growth factor receptor
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IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
ASP/GLUV-RICH (HIGHLY ACIDIC)
PROTEIN KINASE.
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CYTOPLASMIC (POTENTIAL).
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PIR; A41345; TVCHFG.
HSSP; P11362; 1FGK.
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90.7%; Score 97; DB 1; Length 819;

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MEDLINE=91045998; PubMed=2172985;
Musci T.J., Amaya E., Kirschner M.W.;
"Regulation of the fibroblast growth factor receptor in early Xenopus
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50835; IG LIKE; 3.
PROSITE; PS50815; IG LIKE; 3.
PROSITE; PS500107; PROTEIN KINASE DOM; 1.
PROSITE; PS500109; PROTEIN KINASE DOM; 1.
RECEPTOR; PS00109; PROTEIN KINASE TYR; 1.
Receptor; Glycoprotein; Tyrosine-Protein kinase; ATP-binding; Transferase; Phosphorylation; Transmembrane; Immunoglobulin domain;
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FIBROBLAST GROWTH FACTOR RECEPTOR 1.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPIASMIC (FOTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus laevis (African clawed frog).
Enkaryota, Metzoca; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    embryos.",
Proc. Natl. Acad. Sci. U.S.A. 87.8365-8369(1990).
-!- FUNCTION: RECEPTOR FOR BASIC FIBROBLAST GROWTH FACTOR.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
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-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Belongs to the fibroblast growth factor receptor
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01-AUG-1991 (Rel. 19, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Fibroblast growth factor receptor 1 precursor (EC 2.7.1.112).
                                            Indels
Pred. No. 1.1e-08;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                            812 AA.
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L Similarity 90.5
20; Conservative
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01-JUN-1994 (Rel. 29, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Fibroblast growth factor receptor 2 precursor (EC 2.7.1.112) (FGFR-2)
FGFR2 OR BEK OR KSAM.
                                                                                                                                                                                                                                                                                                                                          Gaps
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MEDLINE=91045961; PubMed=2172978;
HOUSSAINT E., Blanquet P.R., Champion-Arnaud P., Gesnel M.C.,
Torrigalia A., Courtois Y., Breathnach R.;
"Related fibroblast growth factor receptor genes exist in the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dionne C.A., Crumley G.R., Bellot F., Kaplow J.M., Searfoss G., Ruta M., Burgess W.H., Jaye M., Schlessinger J.; "Cloning and expression of two distinct high-affinity receptors cross-reacting with acidic and basic fibroblast growth factors."; EMBO J. 9:2685-2692(1990).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                    (POTENTIAL)
(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
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Q9UIH5,
Q9UQH8;
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ISSUB-SCOMEACH cancer;
MEDLINE-90332706; PLUMAGE-2377625;
Hattori Y., Odagiri H., Nakatani H., Miyagawa K., Naito K.,
                                                                                                                                                                                                                                                                                                        87.9%; Score 94; DB 1; Length 812;
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Sabon M., Sasada R., Watanabo T., Ishimaru K., Igarashi K.;
"Two cDNAs encoding novel human FGF receptor.";
Biochim. Biophys. Acta 1089:244-246(1991).
                                                                                                                                                                                                                                                                                                                        Pred. No. 3.6e-08;
3; Mismatches 0; Indels
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Q96KM0;
Q9UIH4;
Q9UQH7;
IG-LIKE C2-TYPE 3.

PROTEIN KINASE.

ATP (BY SINILARITY).

BY SIMILARITY).

-LINKED (GLCNAC. ...) (PC

N-LINKED (GLCNAC. ...) (PC

N-LINKED (GLCNAC. ...) (PC

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P21862; P18443; Q01742; Q12922; Q14300; Q14301;
Q14304; Q14305; Q14672; Q14718; Q14719; Q96KL9;
Q96KW2; Q9NZUZ; Q9NZU3; Q9UD01; Q9UD02; Q9UH3;
Q9UH6; Q9UH7; Q9UH8; Q9UM87; Q9UMC6; Q9UNS7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 87:8180-8184(1990)
                                                                                                                                                                                                                                                                                                                                                                                           SOLAVHKLAKSIPVRROVIVS 426
                                                                                                                                                                                                                                                                                                                                                                          1 HSQMAVHKLAKSIPLRRQVTVS 22
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TISSUB-Neonatal brain stem;
MEDLINE-90360977; PubMed=1697263.
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                                                                                                                                                                                                                                                                          90502 MW;
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nes 19; Conservative
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                                                                                                                                                                                                                                         313
326
812 AA;
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BINDING
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Matches
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"Hepatocyte growth factor (HGF), keratinocyte growth factor (KGF), and their receptors in human breast cells and tissues: alternative
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MEDINE=29108030; PubMed=1309608;
MEDINE=29108030; PubMed=1309608;
Chan A.M.-L., Bottaro D.P., Fleming T.P., Smith C.L., Burgess W.H.,
Chan A.M.-L., Aaronson S.A.;
"Deterermination of ligand-binding specificity by alternative splicing:
Two distinct growth factor receptors encoded by a single gene.";
Proc. Natl. Acad. Sci. U.S.A. 89:246-250(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ueda T., Saski H., Kuwahara Y., Nezu M., Shibuya T., Sakamoto H., Ishii H., Yanagihara K., Mafune K.-I., Makuuchi M., Terada M., "Deletion of the carboxyl-terminal exons of K.sam/FGFR2 by short of specific messenger Ration, generating preferential expression of specific messenger RMAs."; Cancer Res. 59:6080-6086 (1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 3).
Lind D.L., Cox D.R.;
"Sequence and polymorphisms in fibroblast growth factor receptor 2
                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS 7; 9; 10; 11; 12 AND 13), AND VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fibroblast growth factor receptor 2 (FGFR2): genomic sequence and
                                                                                     SEQUENCE FROM N.A. (ISOFORMS 5; 14 AND 15).
MEDLINE-92212948; PubMed=1113574;
Katoh W., Hattori Y., Sasaki H., Tanaka M., Sugano K., Yazaki Y.,
Sugimura T., Terada M.;
"K-sam gene encodes secreted as well as transmembrane receptor
Sakamoto H., Katoh O., Yoshida T., Sugimura T., Terada M.; "K-sam, an amplified gene in stomach cancer, is a member of the heparin-binding growth factor receptor genes."; proc. Natl. Acad. Sci. U.S.A. 87:5983-5987(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS 5; 6; 8; 14 AND 18).
MEDLINE-21845873; PubMed-11856867;
Ingersoll R.G., Paznekas W.A., Tran A.K., Scott A.F., Jiang G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 19).
TISSUB=Breast, and Cornea;
MEDLINE=95170769; PubMed=7866434;
Wilson S.E., Weng J., Chwang E.L., Gollahon L., Leitch A.M., Shay J.W.;
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 3 AND 19), AND VARIANT ARG-613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Steinberger D., Mueller U.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilson S.E., Weng J., Chwang E.L., Gollahon L., Leitch
Shay J.W.;
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                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 89:2960-2964(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytogenet. Cell Genet. 94:121-126(2001);
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. Mol. Biol. Res. 40:707-707(1994).
                                                                                                                                                                                                                                                                                                                                          binding specificity.";
J. Biol. Chem. 267:21225-21229(1992)
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                                                                                                                                                                                tyrosine kinase.";
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Reardon W., Malcolm S.; "Mutations in the third immunoglobulin domain of the fibroblast factor receptor-2 gene in Crouzon syndrome.";
                                             Hum. Mol. Genet. 4:1077-1082(1995).
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MEDLINE=89219016; PubMed=2468999;
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"Expression cDNA cloning of the
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                                                                                                                                                                              Local Similarity 85.7 tes 18; Conservative
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Science 251:72-75(1991).
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MEDLINE=96090259; PubMed=7881378;
GORTY M.C., Preston R.A., White G.J., Zhang Y., Singhal V.K.,
Losken H.W., Parker M.G., Nwokoro N.A., Post J.C., Ehrlich G.D.;
"Crouzon syndrome: mutations in two spliceoforms of FGFR2 and a common point mutation shared with Jackson-Weiss syndrome.";
Hum. Mol. Genet. 4:1387-1390(1995).
                                                                                                                                                                                                        MEDLINE=99214070; PubMed=10196476;
Zhang Y., Gorry M.C., Post J.C., Ehrlich G.D.,
"Genomic organization of the human fibroblast growth factor receptor 2
(FGFR2) gene and comparative analysis of the human FGFR gene family.";
Gene 230:69-79(1999).
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MEDLINE=95179174; PubMed=7874170;
dabs E.W., Li X., Scott A.F., Meyers G.A., Chen W., Eccles M., Mao J.,
Charnas L.R., Jackson C.E., Jaye M.;
"Jackson-Weiss and Crouzon syndromes are allelic with mutations in
fibrolast growth factor receptor 2.";
                                                                                                                                                                               14 AND
                                                                                                                                                                                                                                                                                                SEQUENCE OF 249-313 FROM N.A., AND VARIANTS AS TRP-252 AND ARG-253. MEDLINE-95397814; PubMed=7668257; Mestri N.E., Meyers G.A., Pryburg J.S., Dufresne C., Cohen M.M. Jr., Jabs E.W.; "Analysis of phenotypic features and FGFR2 mutations in Apert syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 251-259 FROM N.A.
MEDLINE=96253074; PubMed=8676562;
Wada C., Ishigaki M., Toyo-oka Y., Yamabe H., Ohnuki Y., Takada F.,
Yamazaki Y., Ohtani H.;
"Nucleotide sequences at intron 6 and exon 7 junction of fibroblast
growth factor receptor 2 and rapid mutational analysis in Apert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95384152; PubMed=7655462;
Oldridge M., Wilkie A.O.M., Slaney S.F., Poole M.D., Pulleyn L.J.,
Rutland P., Hockley A.D., Wake M.J.C., Goldin J.H., Winter R.M.,
               SEQUENCE OF 314-427 FROM N.A.
MEDLINE-20177482; PubMed=10712195;
Glaser R.L., Jiang W., Boyadjiev S.A., Tran A.K., Zachary A.A., Van Malaka A.O.M., Jobnson D., Walsh S., Oldridge M., Wall S.A., Wilka A.O.M., Jabs B.W.;
"Paternal origin of FGFR2 mutations in sporadic cases of Crouzon Syndrome and Pfeiffer syndrome.";
Am. J. Hum. Genet. 66:768-777(2000).
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MEDLINE-96241572; PubMed-8673103;
Moloney D.M., Slaney S.F., Oldridge M., Wall S.A., Sahlin P.,
Stenman G., Wilkie A.O.M.;
"Exclusive parernal origin of new mutations in Apert syndrome.";
Nat. Genet. 13:48-53(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Mutations in the fibroblast growth factor receptor 2 gene cause Crouzon syndrome.";
Nat. Genet. 8:98-103(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANTS CS HIS-340; ARG-342; SER-342; TYR-342 AND CYS-354. MEDLINE=95078932; PubMed=7987400; Reardon W., Winter R.M., Rutland P., Pulleyn L.J., Jones B.M., Malcolm S.;
                                                                                                                                                                               SEQUENCE OF 1-209; 212-767 AND 771-821 FROM N.A. (ISOFORMS 5;
 one in humans."; (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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   gene
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growth
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PIGR2 MOUSE)
P21803; 055141; 000389; 051342;
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 135, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Fibroblast growth factor receptor 2 precursor (EC 2.7.1.112) (FGFR-2)
(Keratinocyte growth factor receptor).
FGFR2 OR ECTI OR BEK.
Mis musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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TISCUB-Brain, and Liver;
MEDLINE-9228073; Pubmed=1373495;
Mansukhani A., Dell'Era P., Moscatelli D., Kornbluth S.,
Hanafusa H., Basilico C.;
Hanafusa H., Basilico C.;
Foraracterization of the murine BEK fibroblast growth factor (FGF)
receptor: activation by three members of the FGF family and
requirement for heparin.";
                                                                                                                       VARIANTS CS GLY-290; TRP-342 AND CYS-354, AND VARIANT JWS ARG-342. MEDLINE=56133301; PubMed=8528214; Bark W.-U., Meyers G.A., Li X., Theda C., Day D., Orlow S.J., Jones M.C., Jabs E.W.; "Novel FGFR2 mutations in Crouzon and Jackson-Weiss syndromes show
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏĘ
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Miki T., Fleming T.P., Bottaro D.P., Rubin J.S., Ron D.,
Aaronson S.A.;
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85.7%; Pred. No. 2.9e-06;
iive 0; Mismatches 3;
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EMBL; M35196; AAA48665.1; -.
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CEK3 CHICK
ID CEK3 CHI
AC P18461;
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         MOI. Cell. Biol. 8:5541-5544(1988).

-!- FUNCTION: RECEPTOR FOR ACIDIC AND BASIC FIBROBLAST GROWTH FACTORS.

POSSESSES A HIGHER APPINITY FOR ACIDIC THAN FOR BASIC FGF'S.

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- ALTERNATIVE PRODUCTS:

Brotn=Alternative splicing; Named isoforms=2;
Name=Long;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                      IsoId=P21803-2; Sequence=VSP_002985, VSP_002986, VSP_002987;
SIMILARITY: Belongs to the fibroblast growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIBROBLAST GROWTH FACTOR RECEPTOR 2. EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS, PRO0109; TYRKINASE.
Probom; PRO0109; TYRKINASE.
Probom; PRO0109; Prot_kinase; 1.
SWART; SMO0219; TYRK; 1.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS50010; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding; Transferase; Phosphorylation; Transmembrane; Signal;
                                                                                                                                                                                                                                                                                                                                              MGD; MGI:9523; Fgfr2.

GO; GO:0007435; P:salivary gland morphogenesis; IMP.
InterPro; IPR00710; Ig-like.
InterPro; IPR00719; Prot_kinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR004245; Tyr_pkinase.
Fam; PF00047; ig; 3.
Pfam; PF00069; pkinase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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EMBL; X55441; CAA39083.1; --
EMBL; M63503; AAA39377.1; --
EMBL; Y16152; CAA76098.1; --
EMBL; Y16167; CAA76099.1; --
EMBL; M23362; AAA37285.1; --
PIR; A44142; TVMSEK.
PIR; S44142; TVMSEK.
PIR; P17255; S17295.
 screening of cDNA libraries.";
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                                                                                                             Name=Short;
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DOMAIN
DOMAIN
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NOMAIN
NP BIND
BINDING
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CARBOHYD
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                                                                                                                                                                                                                       AAGVNTTDEEIBVLYIRNVTPEDAGBYTCLACNSIGISFHS
AWLTVLP -> HSGINSSNAEVLALFNVTEMDAGEYICKVS
NYIGQANQSAWLTVLPKQQ (in isoform Short).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
  C. (POLEMIAL).
AC. (POTENTIAL).
AC. (POTENTIAL).
AC. (POTENTIAL).
NAC. (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pasquale E.B.;
"A distinctive family of embryonic protein-tyrosine kinase
receptors."; Acad. Sci. U.S.A. 87:5812-5816(1990).
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine BDP + protein
tyrosine phosphate.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Belongs to the fibroblast growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              family.
-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77.6%; Score 83; DB 1; Length 821
85.7%; Pred. No. 2.9e-06;
tive 0; Mismatches 3; Indels
                                                                                                                               E -> G (in isoform short).
/FTId=VSP 002985.
Missing (in isoform Short).
/FTId=VSP 002986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Tyrosine kinase receptor CEK3 precursor (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FCDB28ADD61F4414 CRC64;
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A -> V (IN REF. 2).
GE -> RG (IN REF. 2).
E -> R (IN REF. 2).
I -> Y (IN REF. 2).
DV -> R (IN REF. 2).
C -> V (IN REF. 2).
S -> P (IN REF. 2).
W -> R (IN REF. 2).
W -> R (IN REF. 2).
W -> R (IN REF. 2).
W -> R (IN REF. 2).
W -> R (IN REF. 2).
W -> R (IN REF. 2).
W -> R (IN REF. 2).
W -> Y (IN REF. 2).
                                                              N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                     (GLCNAC
                   N-LINKED
N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=90332672; PubMed=2165604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91983 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                            361
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1190
1142
11842
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2229
301
821
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84,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
228
241
265
297
3318
331
                                                                                                                                                                                 38
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RESP, P11362, 146K.

RICEPPO; IPR000710; 19-1ike.

INTERPO; IPR001710; 19-1ike.

RICEPPO; IPR001710; 10-1ike.

RICEPPO; IPR001710; 10-1ike.

RICEPPO; IPR00174; 111 receptor1/11.

RICEPPO; IPR00174; 17-1il receptor1/11.

RICEPPO; IPR00174; 17-1il receptor1/11.

RICEPPO; IPR00174; 17-1il receptor1/11.

RICEPPO; IPR00174; 17-1il receptor1/11.

RICEPPO; IPR00174; 17-1il receptor1/11.

RICEPPO; IPR00174; 17-1il receptor1/11.

RICEPPO; IPR00174; 11-1il receptor1/11.

RICEPPO; IPR00174; 11-1il receptor1/11.

RICEPPO; IPR00174; 11-1il receptor1/11.

RICEPPO; IPR00174; 11-1il receptor1/11.

RICEPPO; IPR00174; 11-1il receptor1/11.

RICEPPO; IPR00174; 11-1il receptor1/11.

RICEPPO; IPR00174; 11-1il receptor1/11.

RICEPPO; IPR00174; IPR00174; II-1il receptor1/11.

RICEPPO; IPR00174; IPR00174; II-1il receptor1/11.

RICEPPO; IPR00174; IPR00174; IPR00174; II-1il receptor1/11.

RICEPPO; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174; IPR00174
MEDLINE=93201992; PubMed=1284237;
Friesel R:, Brown S.A.N.;
Friesel R:, Brown S.A.N.;
Friesel R:, Brown S.A.N.;
Friesel R:, Brown S.A.N.;
Friesel R:, Brown S.A.N.;
Friesel R:, Brown S.A.N.;
Friesel R:, File 1051-1058 (1992).
Friesel R:, File 1051-1058 (1992).
Friesel Receptor for acidic and basic fibroblast growth factors.
Frycsine phosphate.
Frycsine phosphate.
Frycsine phosphate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.0016;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIBROBLAST GROWTH FACTOR EXTRACELLULAR (POTENTIAL)
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (POTENTIAL).
ATP (POTENTIAL).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-)
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82.4%;
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Best Local Similarity
Matches 14; Conserv
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SIGNAL 1
CHAIN 15
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TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DOMAIN
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ACT_SITE
MOD_RES
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CARBOHYD
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CARBOHYD
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          ;
0
                                       InterPro; IPR007110; Ig-like.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR001710; Ig-like.

R InterPro; IPR001719; Proc_kinase.

R InterPro; IPR001245; Proc_kinase.

R InterPro; IPR001245; Proc_kinase.

R InterPro; IPR001045; Proc_kinase.

R InterPro; IPR001045; Proc_kinase.

R Prodom; Pr000001; Proc kinase; 1.

R PR01715; PR00109; TYRKINASE.

R RMART; SM00219; TYRKINASE.

R RMART; SM00219; TYRKINASE.

R RMART; SM00109; TYRKINASE.

R ROSITE; PS00107; PR07EIN KINASE APP; 1.

R ROSITE; PS00109; PR07EIN KINASE DOM; 1.

R ROSITE; PS00109; PR07EIN KINASE DOM; 1.

R ROSITE; PS00109; PR07EIN KINASE TYR; 1.

R ROSITE; PS00109; PR07EIN KINASE TYR; 1.

R ROSITE; PS00109; PR07EIN KINASE TYR; 1.

R RACERSE; PS00109; PR07EIN KINASE TYR; 1.

R RACERSE; PS00109; PR07EIN KINASE TYR; 1.

R RACERSE; PS00109; PR07EIN KINASE TYR; 1.

R RACERSE; PS00109; PR07EIN KINASE TYR; 1.

R RACERSE; PS00109; PR07EIN KINASE TYR; 1.

R RACERSE; PS00109; PR07EIN KINASE TYR; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY)
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
(POTENTIAL)
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01-JUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Fibroblast growth factor receptor 2 precursor (EC 2.7.1.112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CEK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 823;
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PROTEIN KINASE.
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85.7%; Pred. No. 2.9e-06;
ive 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
TYROSINE KINASE RECEPTOR :
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
PHOSPHORYLATION (AUTO-)
POTENTIAL.
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SIMILARITY)
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IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
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(GLCNAC.
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N-LINKED (GLCNAC)
N-LINKED (GLCNAC)
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N-LINKED
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ATP (BY
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AC Q03364;
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SEQUENCE OF 22-4391 FROM N.A., AND VARIANT SJS1 TYR-1532.
MEDLINE=20553141; PubMed=11101850;
Nicole S., Davolne C.-S., Topaloglu H., Cattolico L., Barral D.,
Beighton P., Ben-Hamdia C., Hammouda H., Cruaud C., White P.S.,
Samson D., Urtizberea J.A., Lehmann-Horn F., Weissenbach J.,
Hentati F., Fontaine B.;
"Perlecan, the major proteoglycan of basement membranes, is altered in
patients with Schwartz-Jampel syndrome (chondrodystrophic myotonia).",
Nat. Genet. 26:480-483(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kallunki P., Tryggvason K.;
"Human basement membrane heparan sulfate proteoglycan core protein: a
467-KD protein containing multiple domains resembling elements of the
low density lipoprotein receptor, laminin, neural cell adhesion
molecules, and epidermal growth factor.";
J. Cell Biol. 116:559-571(1992).
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TISSUB=Colon, and Skin;
MEDLINE=92235084; PubMed=1569102;
MEDLINE=92235084; PubMed=1569102;
Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Iozzo R.V.;
"Primary structure of the human heparan sulfate proteoglycan from basement membrane (HSPGZ/perlecan). A chimeric molecule with multiple domains homologous to the low density lipoprotein receptor, laminin, neural call adhesion molecules, and epidermal growth factor.";
J. Biol. Chem. 267:8544-8557(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yi H.F., Iozzo R.V.; "Hepperan of human colon: partial molecular "Hepperan sulfate proteoglycan of human coloning, cellular expression, and mapping of the gene (HSPG2) to the short arm of human chromosome 1.";
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                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91365376; PubMed=1679749;
Dodge_G.R., Kovalszky I., Chu M.L., Hassell J.R., McBride O.W.,
                                                                                                                                                                                            P98160, 016287, Q9H3V5;
01-0CT-1996 (Rel. 34, Created)
28-FBE2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Basement membrane-specific heparan sulfate proteoglycan core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94052171; PubMed=8234307;
Cohen I.R., Graessel S., Murdoch A.D., Iozzo R.V.;
                                                                                                                                                                              PRT; 4391 AA.
                                                                                                                                                                                                                                                                                                              protein precursor (HSPG) (Perlecan) (PLC).
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                       VHKLAKSIPLRRQVTVS
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SEQUENCE FROM N.A.

STATAL=BALB/G; ITSSUE=Spleen;
STRATAL=BALB/G; ITSSUE=Spleen;
MIZULE T.R., Pukita Y. Miyoshi T., Shimizu A., Honjo T.;
MIZULE T.R., Pukita Y. Miyoshi T., Shimizu A., Honjo T.;
MIZULE T.R., Fukita Y. Miyoshi T., Shimizu A., Honjo T.;
MIZULE T.R., Fukita Y. Miyoshi T., Shimizu A., Honjo T.;
Tisolation of cDNA encoding a binding protein specific to 5'-
Dhosphorylated single-stranded DNA with G-rich sequences.";

Nucleic Acids Res. 21:1766-11766 (1993).

-!- FUNCTION: DNA-binding protein specific to 5'-phosphorylated single-stranded guanine-rich sequence related to the immunoglobulin mu chain switch region. Preferentially binds to the motif (5'-GGGCT-3').

-!- SUBCELLULAR LOCAGTION: Nuclear (Potential).

-!- SIMILARITY: Belongs to the DNAZ/NAM7 helicase family.
                                                                                                                                      Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
NOBI_TaxID=10030,
                                               01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
11-FARA-2004 (Rel. 43, Last annotation update)
11-Andraling protein SMUBP-2 (Immunoglobulin MU binding protein 2)
(SMUBP-2) (Cardiac transcription factor 1) (CATF1).
IGHNBP2 OR SMBP-2.
                       STANDARD;
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                       MOUSE
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DNA BIND
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P40694;
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                        R Pfam; PF00057; 1dl_recept_a; 4.

R Pfam; PF01390; SEA; 1.

R PRINTS; RR00261; LDRIRECEPTOR.

R Prodom; PD003031; Laminin_B; 3.

R SMART; SM00180; EGF; Lam; 12.

R SMART; SM00408; IGG2; Lam; 12.

R SMART; SM00408; IGG2; 21.

R SMART; SM00281; LamG; 3.

R SMART; SM00281; LamG; 3.

R SMART; SM00281; LamG; 3.

R SMART; SM00282; LamG; 3.

R SMART; SM00202; EGF 1.

R SMART; SM00202; EGF 1.

R SMART; SM00202; EGF 1.

R PROSITE; PS00202; EGF 2; 6.

R PROSITE; PS00205; LAM G DOMAIN; 3.

R PROSITE; PS00205; LAM G DOMAIN; 3.

R PROSITE; PS00204; SEA; 1.

R PROSITE; PS00204; SEA; 1.

R PROSITE; PS00204; SEA; 1.

R PROSITE; PS00204; SEA; 1.

R PROSITE; PS00204; SEA; 1.

R PROSITE; PS00008; LDLRA_2; 4.

R PROSITE; PS00009; LDLRA_2; 4.

R PROSITE; PS00009; LDLRA_2; 4.

R PROSITE; PS00009; LDLRA_2; 4.

R PROSITE; PS00009; LDLRA_2; 4.

R PROSITE; PS00009; LDLRA_2; 4.

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Pred. No. 29;
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LDL-RECEPTOR CLASS A 1.
LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 3.
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C2-TYPE 3.
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IG-LIKE C2-TYPE 12
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SS DNA-BINDING (BY SIMILARITY).
GLN/PRO-RICH.
POLY-LYS.
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
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# PIR; 335633.

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# PIR; 335633.

# PIR; 335633.

# PIR; 335633.

# PIR; 35603593; AAA ATPase.

# PIR ExPro; IPR001410; DEAD.

# PIR ExPro; IPR001410; DEAD.

# PIR ExPro; IPR001374; R3H.

# PIR ExPro; IPR001374; R3H.

# PIR ExPro; IPR001374; R3H.

# PRO10342; R3H; 1.

# PRART; SM00342; AAAA; 1.

# SMART; SM00343; R3H; 1.

# PRART; SM00154; EAR.

# PRO10154; EAR.

# PIGREAMS; TIGR00376; TIGR00376; 1.

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7; Indels

3; Mismatches

Similarity 47.4 9; Conservative

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1 RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 940-1601 AND 1870-2600 FROM N.A., AND PARTIAL SEQUENCE.

MEDLINE=89034110; PubMed=2972708;

MODIAN D.M., Horigan E.A., Ledbetter S.R., Vogeli G., Sasaki M.,

Yamada Y., Hassell J.R.;

"Identification of CDNA clones encoding different domains of the
basement membrane heparan sulfate proteoglycan.";

"Identification of S3:16379-16389]

"ID BIOL, Chem. 263:16379-16389]

"ID BIOL, Chem. 263:16389]

"ID BIOL, Chem. 26
                                                                                                                                                                                                                                                                                                                                                            Noonan D.M., Fulle A., Valente P., Cai S., Horigan E., Sasaki M., Yanasald Y., Hassell U.R.;
Yamada Y., Hassell U.R.;
"The complete sequence of perlecan, a basement membrane heparan sulfate proteoglycan, reveals extensive similarity with laminin A chain, low density lipoprotein-receptor, and the neural cell adhesion molecule.";
U. Biol. Chem. 266:22939-22947(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- TISSUE SPECIFICITY: Found in the basement membranes.
-i- PTM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL AS N-LINKED AND O-LINKED OLIGOSACCHARIDES.
                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Contains 4 LDL-receptor class A domains.
-!- SIMILARITY: Contains 11 laminin EGF-like domains.
-!- SIMILARITY: Contains 3 laminin IV domains.
-!- SIMILARITY: Contains 15 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 3 laminin G-like domains.
-!- SIMILARITY: Contains 1 EGF-like domains.
-!- SIMILARITY: Contains 1 EGF-like domain.
                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Basement membrane-specific heparan sulfate proteoglycan core protein precursor (HSPG) (Perlecan) (PLC).
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EMBL; J04054; AAA39911.1; -.
EMBL; J04054; AAA39912.1; -.
EMBL; J04054; AAA39912.1; -.
PIR; S18222; S18252.
PDB; 1GL4; Z8-NOV-01.
MGD; MG1:96257; HSPG2.
GO; GO:0005604; C:basement membrane; IDA.
GO; GO:0008104; P:protein localization; IMP.
InterPro; IPR006985; ConA like_lec_gl.
InterPro; IPR006209; EGF like.
InterPro; IPR006209; EGF like.
InterPro; IPR005098; Igg-Ii.
InterPro; IPR005098; Igg-Ii.
InterPro; IPR005098; Igg-Ii.
InterPro; IPR005098; Igg-Ii.
  PRT; 3707 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Extracellular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                   TISSUE=Melanoma;
MEDLINE=92078153; PubMed=1744087;
  STANDARD;
                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
  PGBM_MOUSE
205793;
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JUL-RECEPTOR CLASS A 1.

LUL-RECEPTOR CLASS A 2.

LUL-RECEPTOR CLASS A 3.

LUL-RECEPTOR CLASS A 4.

LUL-RECEPTOR CLASS A 4.

LUL-RECEPTOR CLASS A 4.

LUL-RECEPTOR CLASS A 4.

LUL-RECEPTOR CLASS A 4.

LUL-RECEPTOR CLASS A 4.

LAMININ EGF-LIKE 1 (C-TERMINAL).

LAMININ EGF-LIKE 3.

LAMININ EGF-LIKE 3.

LAMININ EGF-LIKE 5.

LAMININ EGF-LIKE 5.

LAMININ EGF-LIKE 9.

LAMININ EGF-LIKE 9.

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LAMININ EGF-LIKE 11.

LG-LIKE C2-TYPE 2.

LG-LIKE C2-TYPE 9.

LG-LIKE C2-TYPE 9.

LG-LIKE C2-TYPE 12.

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LG-LIKE C2-TYPE 14.

LG-LIKE C2-TYPE 15.

LAMININ G-LIKE C2-TYPE 15.

LG-LIKE C2-TYPE 15.

LAMININ G-LIKE 11.

LG-LIKE C2-TYPE 15.

LAMININ G-LIKE C2-TYPE 15.

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IPR002049; Laminin EGF.
IPR001791; Laminin G.
IPR002172; LDL receptor A.
IPR000082; SEA_domain.
                                                                                                 InterPro; IPR000082; SEA_domain.
Pfam; PF00008; BGF; 4.
Pfam; PF000047; iq; 15.
Pfam; PF00052; laminin B; 3.
Pfam; PF00053; laminin EGF; 7.
Pfam; PF00054; laminin G; 3.
Pfam; PF00154; laminin G; 3.
Pfam; PF001590; SEA; 1.
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EGF-LIKE

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BIRDILNES-25024070, Pub.Med=1926771;
NAVOL N., Pichersky E., Zeidan M., Zamir D., Czosnek H.;
"Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus
                                                                                         with a single genomic component.";
Virology 185:151-161(1991).
-!- SIMILARITY: Belongs to the geminiviruses AL2 protein family.
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-!- SUBUNIT: Monomer (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: Belongs to the dehydroquinate synthase family.
                                                                                                                                                                                                                                                                                                        Query Match 40.7%; Score 43.5; DB 1; Length 135; Best Local Similarity 45.0%; Pred. No. 2.6; Matches 9; Conservative 6; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
3-dehydroquinate synthase (EC 4.2.3.4).
AROB OR BC1517.
Bacillus cereus (strain ATCC 14579 / DSM 31).
Bacteria, Firmicutes; Bacillales; Bacillus.
                                                                                                                                                                                                                                                                           Gemini AL2; 1.
; 15611 MW; F111C8C2F7E9DD32 CRC64;
Tomato yellow leaf curl virus (TYLCV).
Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_TaxID=10832;
                                                                                                                                                                                                                                                                                                                                                                                                                             361 AA
                                                                                                                                                                                                                                          InterPro; IPR000942; Gemini ALZ.
Pfam; PF01444; Gemini ALZ; 1.
PRINTS; PR00230; GEMCÖATALZ.
Probom; PD001117; Gemini ALZ; 1.
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SQVSIKVQHKIAKKKPIRRK 31
                                                                                                                                                                                                                     EMBL; X15656; CAA33689.1; -. PIR; C40779; QQCVC4.
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AROB BACCR
ID AROB BACCR
AC Q81FQ2;
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     LAMININ G-LIKE 2.
LAMININ G-LIKE 3.
LAMININ G-LIKE 3.
HEPARAN SULFATE (POTENTIAL).
HEPARAN SULFATE (POTENTIAL).
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                                                                                                                                                                                                                                                                    Gaps
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MEDLINE=20139435; PubMed=10673335;
Pobl U., Smith J.S., Tachibana I., Ueki K., Lee H.K., Ramaswamy S.,
Wu Q., Mohrenweiser HW., Jenkins R.B., Louis D.N.;
"EHD2, EHD3, and EHD4 encode novel members of a highly conserved
family of EH domain-containing proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Meracaa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               General Section 1972-1975 General and moderately expressed in heart and moderately expressed in placenta, lung, and skeletal muscle.
-!- SIMILARITY: Contains 1 EH domain.
-!- SIMILARITY: Contains 1 EF-hand calcium-binding domain.
                                                                                               HAMAP; MF_00110; -; 1.

InterPro; IPR002658; DHQ_synthase.

Pfam; PF01761; DHQ synthase; 1.

TIGRPAMS; TIGR101357; aroBs; 1.

Aromatic amino acid biosynthesis; Lyase; NAD; Complete proteome. SEQUENCE 361 AA; 39974 MW; E456B4259AA53EDI CRC64;
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40.2%; Score 43; DB 1; Length 361;
Best Local Similarity 36.8%; Pred. No. 9.4;
Matches 7; Conservative 5; Mismatches 7; Indels
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7A95ADAB9C7A76CC CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
EH-domain containing protein 2.
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HAMAP; MF_00110; -; 1.
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Genew; HGNC:3243; EHD2.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Title:	Perfect score	Sequence:

Sequence: 1 HSQMAVHKLAKSIPLRRQVTV Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5 Searched: 1017041 segs, 315518202 residues Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:

	Description	Q9qvxl rattus sp.	Q02063 homo sapien	Q8cfk8 mus musculu	Q9gzm7 mus musculu	Q60830 mus musculu	. Q80t10 mus musculu	Q8n685 homo sapien	Q8cim9 mus musculu	Q60818 mus musculu	Q03836 xenopus lae	Q90z00 brachydanio	Q91897 xenopus lae	Q63827 rattus norv	Q800z0 brachydanio	Q800z1 brachydanio	O9ps96 xenopus lae
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Query Match 100.0%; Score 107; DB 11; Length 203; Best Local Similarity 100.0%; Pred. No. 2.6e-10;

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SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=Breast tumor;
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Eructural domains.";

Science 251:665-688(1991).

REMBL, M638881, AAA3599.1;

RIPR, C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C40862; C408
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QBCFKB,

01-MAR-2003 (TrEMBLrel. 23, Created)

01-MAR-2003 (TrEMBLrel. 25, Last semotation update)

01-OCT -2003 (TrEMBLrel. 25, Last amotation update)

Similar to fibroblast growth factor receptor I (fms-related tyrosine

kinase 2, Pfeiffer syndrome).

Mus musculus (Mouse).

Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
              Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Hou J., Kan M., McKeehan K., McBride G., Adams P., McKeehan W.L.;
"Fibroblast growth factor receptors from liver vary in three
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Heparin-binding growth factor receptor.
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              0; Mismatches
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                                                                                                                                                       76 HSQMAVHKLAKSIPLRRQVTVS 97
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                                                                                                 1 HSOMAVHKLAKSIPLRROVTVS
              22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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TISSUE=Liver;
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STRAIN=balb/C;

MEDLINE=20283643; PubMed=10821861;

MEDLINE=20283643; PubMed=10821861;

Mason I., Vindewoghel L., Gait M.J., Revest J.-M., Duan D.R.,

Mason I., Dickson C., Werner S.;

"Fibroblast growth factor (FGF) receptor 1-IIIb is a naturally

occuring functional receptor for FGFs that is preferentially expressed

"Fibroblast growth factor (FGF) receptor 1-IIIb is a naturally

occuring functional receptor for FGFs that is preferentially expressed

If in the skin and the brain.";

J. Biol. Chem. 275:16091-16097(2000).

RMBL; AR106552; AAF05312.1;

RMSP; PI1652; AAF05312.1;

RMGD; MG1:95522; FGFT..

RMGD; MG1:95522; Pgfr1.

RMGD; MG1:95522; Pgfr1.

RMGD; MG1:95522; Psgr1.

RMGD; MG1:95522; Psgr1.

RMGD; MG1:95522; Psgr1.

RMGD; MG1:95522; Psgr1.

RMGD; RMGD; Pstrain development; IMP.

RMGD; GG:0007420; Pstrain development; IMP.

RMGD; GG:0007435; Pstrain development; IMP.

RMGD; GG:0007435; Pstrain development; IMP.

RMGD; GG:0007435; Pstrain development; IMP.

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                       EMBL, BC033447, AAB334711;

EMBL, BC033447, AAB334711;

EMBL, BC033447, AAB334711;

GO, GO:0005524; F:ATP binding late kinase activity; IEA.

GO; GO:0004674; F:protein-tyrosine kinase activity; IEA.

GO; GO:0004671; F:protein-tyrosine kinase activity; IEA.

R GO; GO:0004687; F:protein-tyrosine kinase activity; IEA.

R GO; GO:0004687; F:protein-tyrosine kinase activity; IEA.

R GO; GO:0004687; F:protein-tyrosine kinase activity; IEA.

R GO; GO:0004687; F:protein-tyrosine kinase activity; IEA.

R GO; GO:000471; F:protein-tyrosine kinase activity; IEA.

R InterPro; IPR003599; IG.

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R InterPro; IPR00359; IG.

R InterPro; IPR003599; IG.

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R InterPro; IPR003599; IG.

R InterPro; IPR003599; IG.

R InterPro; IPR00359; IFRC: I.

R RMART; SM00409; IG; 2.

R RMART; SM00409; IG; 2.

R RMART; SM00219; IFRC: I.

R RMART; SM00219; IFRC: I.

R RMART; RN00119; PROTEIN KINASE ATP; I.

R RROSITE; PS00109; PROTEIN KINASE ATP; I.

R RROSITE; PS00109; RROTEIN KINASE TYR; I.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
VCBI_TaxID=10090;
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Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor receptor 1-IIIb.
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100.0%; Pred. No. 9.5e-10;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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SEQUENCE
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Q80T10;
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Matches
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                                                       Pfam; PF00047; 19; 2.
Pfam; PF00049; pkinase; 1.
Printy: PR00109; TYRKINASE; 1.
Probom; PD000001; Proct kinase; 1.
SMART; SM00219; TYRK; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
ATP-binding; ImmunoglobulIn domaIn; Kinase; Receptor; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning and expression of fibroblast growth factor receptor-1 isoforms in the mouse heart: evidence for isoform switching during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                Indels
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MOST, MAILSOLI, FORT.
MOST, MAILSOLI, FORT.
GO, GO.0007420; P. brain development; IMP.
GO, GO.0004472; P. inner ear morphogenesis; IMP.
GO, GO.0004475; P. Finner ear morphogenesis; IMP.
GO, GO.0007415; P. Finner ear morphogenesis; IMP.
InterPro; IRR00110; IQ-like.
InterPro; IRR00110; IQ-Like.
InterPro; IRR001245; Tyr_pkinase.
InterPro; IRR001245; Tyr_pkinase.
InterPro; IRR001245; Tyr_pkinase.
InterPro; IRR001295.
Pfam; PP00067; Pkinase; I.
PRINTS; PR00100; TYRINASE.
ProDom; PD000001; Prot kinase; I.
SNART; SM00408; IGC2; Z.
SNART; SM0019; TYRKINASE.
PROSITE; PSS0035; IG_LIKE; Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U23445; AACS2183.1; -.
PIR; 149293; 149293.
HSRP; P11367; 1FGK.
                                                                                                                                                                                                                                                                                            Tyrosine-protein kinase.
SEQUENCE 733 AA; 82122 MW; D57EB7642678D293 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor receptor-1, short isoform.
                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 107; DB 11;
100.0%; Pred. No. 9.6e-10;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           733 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  irt development.";
Mol. Cell. Cardiol. 26:1449-1459(1994)
InterPro, IPR000719, Prot kinase.
InterPro, IPR001245, Tyr pkinase.
InterPro, IPR008266, Tyr pkinase_AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     320 HSQMAVHKLAKSIPLRRQVTVS 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Swiss Webster; TISSUE=Heart;
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                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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060830

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SEQUENCE FROM N.A.

GRACHI O', Aizawa K., Akimurat T., Arakawa T., Bono H., Carninci P., Adachi O', Aizawa K., Akimurat T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Haraka T., Hirozane T., Hirozane T., Hirozane T., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kogawa I., Kasukawa T., Katoh H., Kawai J., Kojina Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nomura K., Numurati R., Oho M., Ohsato N., Okazuki Y., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shbata K., Shinagawa A., Shiraki T., Sogabe Y., Tagawa T., Tagawa A., Tanaka T., Tagawa A., Tayawa A., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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STRANIE-STBL/63; IISSUE=Placenta, and Extraembryonic tissue;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
Tyb-binding; Immunoglobulin domain; Kinase; Receptor; Transferase; Tyrosine-protein kinase.
Tyrosine-protein kinase.
PIBROBLAST GROWTH FACTOR RECEPTOR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
d days pregnant adult female placenta and extra embryonic tissue
CDNA, RIKEN full-length enriched library, clone;383040Hf21
product:fibroblast growth factor receptor 1, full insert
                                                                                                                                                                                                   FIBROBLAST GROWTH FACTOR RECEPTOR-1, SHORT ISOFORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 107; DB 11; Length 733; 100.0%; Pred. No. 9.6e-10; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Placenta, and Extraembryonic tissue;
RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Extraembryonic tissue;
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MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                           23F35C024C3DE7B6 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320 HSOMAVHKLAKSIPLRROVTVS 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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STRAIN=C57BL/6J; TISSUE=Placenta,
MEDLINE=20499374; Pubmed=11042159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "High-efficiency full-length cDN
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                               733 AA; 82168 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
les 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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activity; IEA

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Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

B. Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

B. Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

B. Schools (Jule-2001) to the EMBL/GenBank/DDBJ databases.

B. Schools (Jule-2001) to the EMBL/GenBank/DDBJ databases.

B. Stratesper Exprotein serine/threconine kinase activity; IEA.

CO; GO:00046713 F: Protein serine/threconine kinase activity; IEA.

R. Sp. Sprotein amino acid phosphorylation; IEA.

B. Sprotein amino acid phosphorylation; IEA.

B. Sprotein amino acid phosphorylation; IEA.

InterPro; IPR003599; IG.

R. InterPro; IPR003599; IG.

R. InterPro; IPR003599; IG.

R. InterPro; IPR001249; Protekinase.

R. InterPro; IPR001245; Prockinase.

R. Pron; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; Protocol; R. SMART; SMO0409; IG; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 25, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
similar to fibroblast growth factor receptor 1.
Was musculus (Mouse).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
(VCBI_TaxID=10090;
GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004674; F:protein serine/threonine kinase activity; IEB.

GO; GO:0004713; F:protein serine/threonine kinase activity; IEB.

R GO; GO:0004712; F:receptor activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

R GO; GO:0016740; F:transferase activity; IEA.

IN InterPro; IPR001599; IG-1ike.

IN InterPro; IPR001599; IG-2.

IN InterPro; IPR001599; IG-2.

IN InterPro; IPR001599; Prot kinase.

IN InterPro; IPR001599; Prot kinase.

IN PROMO17; IG; 3.

PROMO17; IG; 3.

PROMO17; SM00409; IG; 3.

R RMART; SM00109; TYRKINASE.

R PROSITE; PS50010; PROTEIN KINASE DAP; 1.

R PROSITE; PS50011; PROTEIN KINASE DAP; 1.

R PROSITE; PS50011; PROTEIN KINASE DAP; 1.

R PROSITE; PS50011; PROTEIN KINASE DAP; 1.

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R PROSITE; PS50011; PROTEIN KINASE DAP; 1.

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R PROSITE; PS50011; PROTEIN KINASE DAP; 1.

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R PROSITE; PS50011; PROTEIN KINASE DAP; 1.

R PROSITE; PS50011; PROTEIN KINASE DAP; 1.

R PROSITE; PS50011; PROTEIN KINASE DAP; 1.

R PROSITE; PS50011; PROTEIN KINASE DAP; 1.

R PROSITE; PS50011; PROTEIN KINASE DAP; 1.
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100.0%; Score 107; DB 4; Length 820;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 407 HSQMAVHKLAKSIPLRRQVTVS 428
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               Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome).
Homo sapiens (Human).
                                                                                                                                                                                                                  MEDLINE=CSTBL/GJ, TISSUE=Placenta, and Extraembryonic tissue;
MEDLINE=CSTBL/GJ, TISSUE=Placenta, and Extraembryonic tissue;
MEDLINE=CSTBL/GJ, TISSUE=Placenta, T. Sashino H., Akiyama J., Nishi K., Kitsunai T., Tashino H., Itoh M.,
Sumi N., Ishi Y., Nakamura S., Hazama M., Nishino T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiwi M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanka T., Matsuura S., Kawai J.,
Ckazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
Sequencing pipeline with 384 multicapillary sequencer.",
Genome Res. 10:1757-1771 (2000)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SMART; SM00409; IG; 2.
SMART; SM00200; 2.TKC; 1.
SMART; SM00129; TyrKC; 1.
PROSITE; PSS0835; IG LIKE; 2.
PROSITE; PSS00107; PROTEIN KINASE ATP; 1.
PROSITE; PSC00109; PROTEIN KINASE TYR; 1.
SEQUENCE 733 AA; 82211 MW; 50E95FE644692528 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               820 AA.
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Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Prot_kinase; 1.
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ses 22; Conserv
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SEQUENCE FROM N.A.
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BMBL; U22324; AAC52182.1; ---
BMBL; U22324; AAC52182.1; ---
BMBL; U22324; AAC52182.1; ---
BMSP; P11362; 149289.

R HSSP; P11362; 1872.

MGD; MGI:95522; Fgfr1.

R GO; GO:0007435; P:salivary gland morphogenesis; IMP.

GO; GO:0007435; P:salivary gland morphogenesis; IMP.

GO; GO:0007435; P:salivary gland morphogenesis; IMP.

GO; GO:0007435; P:salivary gland morphogenesis; IMP.

InterPro; IPR00119; Prot kinase.

InterPro; IPR00129; Prot kinase.

InterPro; IPR0019; Prot kinase; 1.

R Ffam; PR00109; PRXINASE.

R PROSTITE; PR00107; PROTEIN KINASE DOW; 1.

R PROSTITE; PR00107; PROTEIN KINASE DOW; 1.

R PROSTITE; PR00107; PROTEIN KINASE DOW; 1.

R PROSTITE; PR00107; PROTEIN KINASE DOW; 1.

R PROSTITE; PR00107; PROTEIN KINASE DOW; 1.

R PROSTITE; PR00107; PROTEIN KINASE TYR; 1.

R PROSTITE; PR00107; PROTEIN KINASE TYR; 1.

R PROSTITE; PR00107; PROTEIN KINASE TYR; 1.

R PROSTITE; PR00107; PROTEIN KINASE TYR; 1.

R PROSTITE; PR00107; PROTEIN KINASE TYR; 1.

R PROSTITE; PR00107; PROTEIN KINASE TYR; 1.

R ATP-binding; Immunoplobulin domain; Kinase; Receptor; Transferase;

Tyrosine-protein kinase.
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                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Swiss Webster; TISSUE=Heart; MEDLINE=95205422; PubMed=7897669; Mid Y., Pasumarthi K.B., Bock M.B., Lytras A., Kardami E., Cattini P.A.; "Cloning and expression of fibroblast growth factor receptor-1 isoforms in the mouse heart: evidence for isoform switching during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musimus; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                             .
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                                                                                                                                                                                                                                                                             100.0%; Score 107; DB 11; Length 820; 100.0%; Pred. No. 1.1e-09;
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                 820 AA; 91668 MW; 58319BDB3EEA9D34 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor receptor-1, long isoform.
FGFR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             822 AA.
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SMART; SM00220; S_TKC; 1.
SMART; SM00219; TYTKC; 1.
PROSITE; PSS00107; PROTEIN KINASE ATP; 1.
PROSITE; PSS0011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            HSQMAVHKLAKSIPLRRQVTVS 428
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Jin Y.;
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                                                                                                                                                                                                                                                                                                             Local Similarity 100.
nes 22; Conservative
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                                                                                                                                                                                       Receptor.
SEQUENCE
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Q60818;
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R GO; GO: 0005524; F:ATP binding; IEA.
GO; GO: 0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO: 0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO: 0004672; F:receptor activity; IEA.
GO; GO: 0006468; P:protein amino acid phosphorylation; IEA.
GO; GO: 0006468; P:protein amino acid phosphorylation; IEA.
GO; GO: 0006468; P:protein amino acid phosphorylation; IEA.
GO; GO: 0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR000719; Protein amino acid phosphorylation; IEA.
InterPro; IPR000719; Protein kinase.
R InterPro; IPR0008056; Tyr_pkinase.
R InterPro; IPR0008056; Tyr_pkinase.
R Propom; Pr000601; Protein kinase; I.
R RAMAT; SM00109; Protein kinase; I.
R RAMAT; SM00109; PROTEIN KINASE ATP; I.
R PROSITE; PS00109; PROTEIN KINASE DOM; I.
R PROSITE; PS00109; PROTEIN KINASE TYR; I.
M ATP-binding; Immunoglobulin domain; Kinase; Receptor; Signal; Transferase; Tyrosine-protein kinase.
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22 724 FIBROBLAST GROWTH FACTOR RECEPTOR
724 AA, 80889 MW; 036D35842ED5BDB3 CRC64;
  Length 822;
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                                               Indels
                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor receptor precursor.
100.0%; Score 107; DB 11;
100.0%; Pred. No. 1.1e-09;
ive 0; Mismatches 0;
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(TrEMBLrel. 19, Last sequence update)
                                                                                                                   409 HSQMAVHKLAKSIPLRRQVTVS 430
                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog)
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                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                         1 HSQMAVHKLAKSIPLRRQVTVS 22
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                                               Conservative
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                                                                                                                                                                                                                                                PRELIMINARY;
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Best Local Similarity
Local 20; Conserva
Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8355;
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01-DEC-2001 (
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ID OO
AC OO
DT OO
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rođentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                    HESP; PULLSG2; AS 752.

RESP; PULLSG2; AS 752.

RESP; PULLSG2; AS 752.

RESP; PULLSG2; FEATP binding; IEA.

RO; GO:0006468; F:Protein amino acid phosphorylation; IEA.

RO; GO:0006468; P:Protein amino acid phosphorylation; IEA.

RO; GO:0006468; P:Protein amino acid phosphorylation; IEA.

RICHEPPO; IPRO013598; IG-11ke.

RICHEPPO; IPRO013598; IG-11ke.

RICHEPPO; IPRO01359; Prot_kinase.

RICHEPPO; IPRO01359; Prot_kinase.

RICHEPPO; IPRO01359; Prot_kinase.

REMINES; PRO0109; Prot_kinase, 1.

REMINES; PRO0109; Prot_kinase, 1.

REMINES; PRO0109; PROTEIN KINASE APP; 1.

REMINES; PRO1019; PROTEIN KINASE APP; 1.

REMINES; PRO1019; PROTEIN KINASE APP; 1.

REMINES; PRO1019; PROTEIN KINASE APP; 1.

REMINES; PRO1019; PROTEIN KINASE APP; 1.

REMINES; PRO1019; PROTEIN KINASE APP; 1.

REMINES; PROSITE; PROTEIN KINASE APP; 1.

REMINES; PROSITE; PROTEIN KINASE APP; 1.
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WEDLINE-93158788; PubMed=8381605;
XEDLINE-93158788; PubMed=8381605;
XEDLINE-93158788; PubMed=8381605;
XEDLINE-93158788; PubMed=8381605;
XEDLINE-9315878; Revent H.M.; Burnow, C.R.; Ballermann B.J.;
XEDLINE-9315878; Revent H.M.; Burnow, Gevelopment.";
XEDLINE-9815187; Refe-F73(1993).
XEDLINE, S54008; AA554274.1;
XEDLINE, S54008; AA554274.1;
XEDLINE, S54008; AA554274.1;
XEDLINE, S54008; AA554274.1;
XEDLINE, S6705; A56795.
XEDLINE, S670524; REAL Binding; IEA.
XEDLINE, S670524; REAL BINDING; IEA.
XEDLINE, S670524; REAL BINDING; IEA.
XEDLINE, S670524; REAL BINDING; IGA.
XEDLINE-PRO; IPRO00110; IG-11ke.
XEDLINE-PRO; IPRO00119; PEOC Kinase.
XEDLINE-PRO; IPRO001245; TYL_DKinase.
XEDLINE-PRO; IPRO01245; TYL_DKinase.
XEDLINE-PROD1245; TYL_DKinase.
XEDLINE-PRO01245; TYL_DKINASE.
XEDLINE-PRO01245; TYL_DKINASE.
XEDLINE-PRO01245; TYL_DKINASE.
XEDLINE-PRO01245; TYL_DKINASE.
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XEDLINE-PRO01245; TYL_DKINASE
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CHAIN 22 814 FIBROBLAST GROWTH FACTOR RECEPTOR.
SEQUENCE 814 AA; 90681 MW; B47CE05F0A8F962A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

90.7%; Score 97; DB 13; Length 814;
Best Local Similarity 90.9%; Pred. No. 5.8e-08;
Matches 20; Conservative 2; Mismatches 0; Indels
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01-NOV-1996 (TrEMBirel. 01, Last sequence update)
01-NOV-1996 (TrEMBirel. 21, Last sequence update)
01-0CT-2003 (TrEMBirel. 25, Last annotation update)
Pibroblast growth factor receptor 1 beta-isoform.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            729 AA.
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Dev. Dyn. 203:119-140(1995).
EMBL; M55163; AAA49990.1; -.
EMBL; U11723; AAA91286.1; -.
PIR; A39752; A39752.
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Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tyrosine-protein kinase.
SIGNAL
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MEDLINE-95383727; PubMed-7655077;
Brandli A.W., Kirschner M.W.;
"Molecular cloning of tyrosine kinases in the early Xenopus embryo:
identification of Eck-related genes expressed in cranial neural crest cells of the second (hyoid) arch.";
                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0109; TYRKINASE.
Probom; PRO01001; Prot kinase; 1.
SMART; SM00408; IGC2; 3.
SMART; SM00209; TYRK.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS50017; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
ATP-binding; Immunoglobulin domain; Kinase; Receptor; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                                                        Groth C., Scholpps., Lardelli M., Brand M.;

"Expression analysis of zebrafish fgfr1 isoforms";

"Expression analysis of zebrafish fgfr1 isoforms";

Exbritted (JUN-201) to the EMBL/GenBank/DDBJ databases.

EMBL; AF38440; AAK64494.1; -...

EMBL; AF38440; APD binding; IEA.

GO: GO:00064713; F:procein-tyrosine kinase activity; IEA.

GO: GO:00164713; F:procein-tyrosine kinase activity; IEA.

GO: GO:00164713; F:procein-activity; IEA.

GO: GO:00164872; F:receptor activity; IEA.

GO: GO:0016481; P:procein-amino acid phosphorylation; IEA.

R GO: GO:0016488; P:procein-amino acid phosphorylation; IEA.

R INTERPRO; IPR003199; IEQ-C2.

R INTERPRO; IPR003199; Prot Kinase.

R INTERPRO; IPR003245; Tyr_pkinase.

R INTERPRO; IPR003266; Tyr_pkinase.

R Pfam; PF00047; Lg; 3.

R Pfam; PF00047; Lg; 3.

R Pfam; PF00047; Lg; 3.
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Friesel R.E., Dawid I.B.;
Submitted (AUG-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tyrosine-protein kinase.
SEOUENCE 806 AA; 90489 MM; 056AF51FEAB0FBF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor receptor precursor.
XIFGFR OR E59.
             01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                       Brachydanio rerio (Zebrafish) (Danio rerio).
                                               Fibroblast growth factor receptor 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        392 NSQLAVHKLAKSIPLRRQVTVS 413
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nes 20; Conservative
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NCBL_TaxID=8355;
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                                                                                                                                                                                                                                                                                           NCBI_TaxID=7955;
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RESULT 12 Q91897

Matches

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Receptor.
SEQUENCE
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Brkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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Best Local Similarity 85.7%; Pred. No. 1.3e-06;
Matches 18; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                       Query Match

88.8%; Score 95; DB 11; Length 729;
Best Local Similarity 95.0%; Pred. No. 1.1e-07;
Matches 19; Conservative 1; Mismatches 0; Indels
ProDom; PD000001; Frot kinase; 1.
SMART; SM00408; IGC2; 2.
SNART; SM00219; TyrKc; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS50011; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE_DOM; 1.
ATP-binding; Immunoglobulin domain; Kinase; Transferase; Tyrosine-protein kinase.
Tyrosine-protein kinase.
SEQUENCE 729 AA; 81627 MW; C19DFDAFFD5BAOBF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Fibroblast growth factor receptor 1 isoform 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  756 AA
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SEQUENCE
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Q800Z0
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                  090021,
090021,
090021,
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Forming growth factor receptor 1 isoform 2.
Forming rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Actinopterygii, Meopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NOBI TaxiD=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Groth C., Scholpp S., Brand M., Lardelli M.;

"Developmental expression of zebrafish fgfr1.";

Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

BMBL, AN197498; AA045658.1;

EMBL, AN197498; AA045658.1;

GO; GO:00004674; F:protein serine/threonine kinase activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:00044882; F:receptor activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
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83.2%; Score 89; DB 13; Length 80
Best Local Similarity 85.7%; Pred. No. 1.4e-06;
Matches 18; Conservative 3; Mismatches 0; Indels
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804 AA.
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InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003598; IG.
InterPro; IPR003298; IG.
InterPro; IPR003290; Ser_thr_pkinase.
InterPro; IPR003269; Ser_thr_pkinase.
InterPro; IPR003266; Tyr_pkinase.
InterPro; IPR003269; Tyr_INTERIOR INTERIOR 
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      PRELIMINARY;
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10, Appl
13345, A
13345, A
5, Appl;
7, Appl;
3143, Appl
30297, A
32541, Ap
16, Appl
2604, Appl
2604, Appl
2604, Appl
2604, Appl
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APPLICANT: Walerer, Michael C.
APPLICANT: Walerer, Pablo D.T.
APPLICANT: Barr, Philip J.
TITLE OF INVENTION: Expression and Use of Human Fibroblast
TITLE OF INVENTION: Growth Factor Receptor
TITLE OF INVENTION: Growth Factor Receptor
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSED: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STRYE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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MEDLUM TYPE: Floppy disk
COMPUTER: BN PC compatible
COMPUTER: BN PC compatible
CORPUTER: BN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.25
SOSTWARE: Patentin Release #1.0, Version #1.25
CURRINT APPLICATION DATE:
APPLICATION NUMBER: US/07/640,029
FLING DATE: 19910111
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
RETERRATION NUMBER: GH-165
TELEPHONE: 510-601-2708
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TELEPHONE: 510-601-2708
TELEPHONE: 510-601-2708
TELEPHONE: 510-601-2708
TELEPHONE: STO-601-2708
US-08-070-165F-10

US-08-471-570-4

US-08-471-570-4

US-09-489-039-13345

US-09-489-039-13345

US-09-489-039-17924

US-09-185-198-5

US-09-115-824-7

US-09-115-824-7

US-09-252-991A-30297

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Best Local Similarity 100.0%; Pred. No. 9.1e-10;
Matches 22; Conservative 0; Mismatches 0;
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; Sequence 3, Application US/07640029
; Patent No. 5229501
; GENERAL INFORMATION:
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                                                   GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-07-921-807B-6
US-08-439-992A-4
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US-08-441-1570-8
US-08-441-1570-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               389414 segs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-757-415A-3
107
1 HSQWAVHKLAKSIPLRRQVTVS 22
                                                                                                                                                                                                                 - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
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APPLICATION NUMBER: US/08/441,944A
PILING DATE: 16-MAY-1995
CLASSPICATION NUMBER: US/08/441,944A
PRICATION S10
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/921,807
FILING DATE: 29-58P-1992
ATTORNEY/AGBNT INFORMATION:
NAME: MCCLUNG, BARBARA G.
REGISTATION NUMBER: 31,131
REFERENCE/DOCKET NUMBER: 0209.001
TELEPHONE: (510) 601-2708
TELEPHONE: (510) 601-2708
TELEPAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 731 amino acids
TYPE: amino acids
    UMBER: US/08/441,944A
16-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 HSQMAVHKLAKSIPLRRQVTVS 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 HSQMAVHKLAKSIPLRRQVTVS 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 731 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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                                                           Sequence 5, Application US/07921807B
Patent No. 5474914
GENERAL INFORMATION:
APPLICANT: SPAETE, RICHARD
TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION
TITLE OF INVENTION: OF VIRAL PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: CHIRON CORPORATION
STREET: 4550 Horton Street - R440
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                             COUNTRY: USA

CONFUTER PAGABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: IBM PC compatible
OMPUTER: PLOPS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,807B
FILING DATE: 29-SEP-1992
CLASSIPFCATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METHOD OF INCREASING EXPRESSION OF VIRAL PROTEINS 20
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-441-944A-5
US-08-441-944A-5
Sequence 5. Application US/08441944A
Patent No. 576720
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
MUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: 4550 Horton Street - R440
CITY: Emeryville
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: MCCLUNG, BARBARA G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0209.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 661-2708
TELEPHONE: (510) 652-3542
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           318 HSQMAVHKLAKSIPLRRQVTVS 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 HSQMAVHKLAKSIPLRRQVTVS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            731 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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; Sequence 3, Application US/08439992A
; Patent No. 625454
; Patent INFORMATION:
; APPLICANT: Fifer, Michael C.
; APPLICANT: Pablo, Valenzuela D.T.
; APPLICANT: Philip, Barr J.
; TITLE OF INVENTION: Expression and Use of Human Fibroblast
; TITLE OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
Query Match
Best Local Similarity 100.0%; Pred. No. 9.2e-10;
Matches 22; Conservative 0; Mismatches 0: Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,992A
FILING DATE: 12-MAY-1995
CLASSIFICATION: 530
ATTORNEY, AGENT INFORMATION:
NAME: Chung, Ling-Fong
REGISTRATION NUMBER: 0165.004
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 0165.004
TELECOMMUNICATION NUMBER: 0165.004
TELECOMMUNICATION NUMBER: 0165.004
TELECOMMUNICATION NUMBER: 0165.004
TELECOMMUNICATION NUMBER: 0165.354
TELECOMMUNICATION NUMBER: 0165.354
INFORMATION FOR SEQ ID NO: SEQUENCE CHRRACTERISTICS: SEQUENCE CHRRACTERISTICS:
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ADDRESSEE: CHIRON CORPORATION
STREET: 4560 Horton Street - R440
                                            Emeryville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-921-807B-6
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100.0%; Score 107; DB 1; Length 733;
Best Local Similarity 100.0%; Pred. No. 9.2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels
                                            100.0%; Score 107; DB 3; Length 731; 100.0%; Pred. No. 9.2e-10; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kiefer, Michael C.
APPLICANT: Valenzuela, Pablo D.T.
APPLICANT: Valenzuela, Pablo D.T.
APPLICANT: Barr, Philip J.
TITLE OF INVENTION: Expression and Use of Human Fibroblast
TITLE OF INVENTION: Growth Factor Receptor
NUMBER OR SEQUENCES: 12
CORRESPONDENCE 12
ADDRESSE: Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:

ZIP: 94608
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/640,029
FILING DATE: 19910111
CLASSIFICATION: 530
ATTORNEY/ACENT INDER: CH-165
REGISTRATION NUMBER: CH-165
REFERENCE/DOCKET NUMBER: CH-165
TELEFAX: 510-601-2708
TELEFAX: 510-601-2708
TELEFAX: 510-601-2708
TELEFAX: 510-655-3542
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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Patent No. 5474914
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
METHOD OF INCREASING EXPRESSION
TITLE OF INVENTION:
OF VIRAL PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320 HSQMAVHKLAKSIPLRRQVTVS 341
                                                                                                                                                                                         318 HSOMAVHKLAKSIPLRROVTVS 339
                                                                                                                                             1 HSQMAVHKLAKSIPLRRQVTVS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Bmeryville
STATE: California
                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/07640029
Patent No. 5229501
GENERAL INFORMATION:
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TYPE: AMINO ACID
STRANDEDNESS: single
                                               Query Match
Best Local Similarity 100.0
Matches 22; Conservative
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; MOLECULE TYPE: peptide
US-07-640-029-4
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US-07-921-807B-6
       US-08-439-992A-3
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US-07-640-029-4
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Pred. No. 9.2e-10;
Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/441,944A
FILING DATE: 16-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/921,807
FILING DATE: 3-5-SEP-1992
ATTORNEY/AGENT INFORMATION:
COUNTRY: USA

ZIP: 94608-2916
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/921,807B
FILING DATE: 29-SEP-1992
CLASSIFICATION NUMBER: US/07/921,807B
FILING DATE: 29-SEP-1992
CLASSIFICATION NUMBER: 0209.001
FELECOMMUNICATION INFORMATION:
TELEPATION NUMBER: 33.113
REFERENCE/DOCKET NUMBER: 0209.001
TELEPAX: (510) 601-2708
TELEPAX: (510) 665-3542
INFORMATION POR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
CLENGTH: 733 anaho acids
TYPE: anaho acids
TYPE: Anaho acids
TYPE: Anaho acids
TYPE: Anaho acids
TYPE: Anaho acids
TYPE: Anaho acids
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APPLICANT: SPAETE, RICHARD
TILLE OF INVENTION: WETHOD OF INCREASING EXPRESSION
TITLE OF INVENTION: OF VIRAL PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
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REFERENCE/DOCKET NUMBER: 0209.001
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     320 HSOMAVHKLAKSÍPLRROVTVS 341
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; Sequence 6, Application US/08441944A
; Patent No. 5767250
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100.0%; Pr
tive 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: MCCLUNG, BARBARA G
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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RESULT 10
US-07-640-029-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Stefer, Michael C.
APPLICANT: Pablo, Valenzuela D.T.
APPLICANT: Philip, Barr J.
TILLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 12
ADDRESSEE: Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTEXT: CLEAR STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE ST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-439-992A-4
; Sequence 4, Application US/08439992A
; Patent No. 6255454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEE: Chiron Corporation: 4560 Horton Street Emeryville
TELEPRA: (510) 601-2708
TELEPRA: (510) 655-3542
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 733 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein US-08-439-992A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                US-08-441-944A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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320 HSQMAVHKLAKSIPLRRQVIVS 341

RESULT 9

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Sequence 1, Mglication Us/O764029
Sequence 1, Mglication Us/O764029
Septication Us/O764029
Septication Useparation
Septication Sequence 1, Marchael C.
APPLICANT: Kaffer, Mchael C.
APPLICANT: Malancia, Pablo D.T.
APPLICANT: Malancia, Pablo D.T.
APPLICANT: Malancia, Pablo D.T.
APPLICANT: Malancia, Pablo D.T.
APPLICANT: Malancia, Pablo D.T.
APPLICANT: Malancia, December 1, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Malancia, Mal
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100.0%; Score 107; DB 1; Length 820; 100.0%; Pred. No. 1e-09; Live 0; Mismatches 0; Indels
                                                                                                                                                              US-08-441-944A-3
Sequence 3, Application US/08441944A
Sequence 3, Application US/08441944A
Sequence 3, Application US/0844194A
FIRE NO. 576726
FIRESTAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CORRESPONDENCE 20
CORRESPONDENCE ADDRESS:
ADDRESSE: CHIRON CORPORATION
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppw disk
MEDIUM TYPE: Floppw disk
MEDIUM TYPE: Floppw disk
COMPUTER: IBM PC Compatible
COMPUTER: BATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,944A
FILING DATE: 16-MAY-1995
CLASSIFICATION NUMBER: 3307/921,807
ATTORNEY/AGENT INFORMATION:
NAME: MCCLUNG, BARBARA G.
NEGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 33,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Leder, Philip
TITLE OF INVENTION: SYSTEM FOR ASSAYING BINDING
TITLE OF INVENTION: TO A HEPARIN-BINDING GROWTH
TITLE OF INVENTION: FACTOR RECEPTOR
NUMBER OF SEQUENCES: 6
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       407 HSQMAVHKLAKSIPLRRQVTVS 428
                                                                                 407 HSQMAVHKLAKSIPLRRQVTVS 428
                                             1 HSQMAVHKLAKSIPLRRQVTVS 22
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Patent No. 5789182
GENERAL INFORMATION:
APPLICANT: Yayon, Avner
APPLICANT: Caritz, David M.
APPLICANT: Ladsbrun, Michael
APPLICANT: Leder, Philip
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TELEPAK: (510) 655-3542
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 820 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 22; Conservative
    22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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US-08-166-717D-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-441-944A-3
      Matches
                                                                                                                                               RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 107; DB 1; Length 817; Best Local Similarity 100.0%; Pred. No. 1e-09; Matches 22; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 107; DB 1; Length 820; Pred. No. 1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/07921807B
Patent No. 5474914
GENERAL INFORMATION:
TITLE OF INVENTION: METHOD OF INCREASING EXPRESSION
TITLE OF INVENTION: OF VIRAL PROTEINS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: CHIRON CORPORATION
STREET: 4560 Horton Street - R440
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/640,029
FILING DATE: 19910111
                                                                               CLASSIFICATION: 530
ATTORNEY/AGENT INPORMATION:
NAME: MCCLUNG, BArbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: CH-165
TELECHOMINICATION IFFORMATION:
TELEPHONE: 510-601-2708
TELEPHONE: 510-601-2708
TELEPHONE: 510-655-3542
INFORMATION FOR ERQ ID NO: 2:
SQUENCE CHARACTERISTICS:
LENGTH: 817 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           409 HSOMAVHKLAKSIPLRROVTVS 430
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-07-921-8078-3
                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: peptide US-07-640-029-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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Best Local Similarity
                                                                FILING DATE: 19
CLASSIFICATION:
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US-07-921-807B-3
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407 HSQMAVHKLAKSIPLRRQVTVS 428
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                     REFERENCE/DOCKET NUMBER: 0165.
TELECHANICATION INFORMATION:
TELEPHONE: 510-923-2704
TELEPHONE: 510-923-2704
TELEPHONE: 510-923-2704
TELEPHONE: 610 655-3542
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 820 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: mino acid
TYPE: mino acid
TYPE: mino acid
TYPE: mino acid
TYPE: mino acid
TYPE: protein
US-08-439-992A-1
       36,482
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amino acid
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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       REGISTRATION NUMBER:
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Best Local Similarity
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US-07-997-133-1
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100.0%; Score 107; DB 1; Length 820;
Best Local Similarity 100.0%; Pred. No. 1e-09;
Matches 22; Conservative 0; Mismatches 0; Indels
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Sequence 1, Application US/0843992A

GENERAL INFORMATION:
APPLICANT: Kiefer, Michael C.
APPLICANT: Pablo, Valenzuela D.T.
APPLICANT: Philip, Barr J.
TITLE OF INVENTION: Expression and Use of Human Fibroblast
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSED: Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patentin Release #1.0, Version #1.30
                                                                                       STATE: Massachusetts
COUNTXY: U.S.A.
ZIP: 02110
ZONPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WATGPERFECT (Version 7.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/166,717D
FILING DATE: 12/14/93
CLASSIFTCATION: 435
PRIOR APPLICATION NUMBER: 07/631,717
APPLICATION NUMBER: 07/631,717
FILING DATE: 12/20/90
ATTORNEY/AGENT INFORMATION:
NAME: Kristina Bicker-Brady
REGISTRATION NUMBER: 39,109
BERGISTRATION NUMBER: 39,109
BERGISTRATION NUMBER: 39,109
BERGISTRATION NUMBER: 07/631,717
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APPLICATION NUMBER: US/08/439,992A
FILING DATE: 12-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  407 HSQMAVHKLAKSIPLRRQVTVS 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Police
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 HSQMAVHKLAKSIPLRRQVTVS 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 00 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (617) 723-4123
TELEFAX: (617) 723-8962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Chung, Ling-Fong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
US-08-166-717D-6
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US-08-439-992A-1
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Length 820;
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Pred. No. 1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/07997133
Fatent No. 5288855
GENERAL INFORMATION:
APPLICANT: Mazue, Guy
APPLICANT: Racchi, Antonella
APPLICANT: Racchi, Antonella
APPLICANT: Ramiencos, Paolo
TITLE OF INVENTION: Extracellular Form of the Human
TITLE OF INVENTION: Fibroblast Growth Factor Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OBLON, SPIVAK, MCCLELLAND, MAIBR & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: CDCM, SITMAN, NOTELLIAND, FORTH ADDRESSEE: CDCM, SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMAN SITMA
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Query Match 100.0%; Score 107; DB 3; Best Local Similarity 100.0%; Pred. No. 1e-09; Matches 22; Conservative 0; Mismatches 0;
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0; Gaps

Matches 22; Conservative 0; Mismatches 0; Indels

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Search completed: August 2, 2004, 09:32:29 Job time : 5.19737 secs

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OM protein - protein search, using sw model Run on:

(without alignments) 588.640 Million cell updates/sec August 2, 2004, 09:31:19; Search time 11.7237 Seconds

US-09-757-415A-3 Title: Perfect score:

1 HSQMAVHKLAKSIPLRRQVTVS 22 Seguence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1291235 seqs, 313682936 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:*

| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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| cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
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| cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 3, Appli	Sequence 47, Appl		Sequence 714, App	Sequence 714, App	Sequence 42, Appl	Sequence 2, Appli	Sequence 8, Appli	Sequence 2, Appli	Sequence 26, Appl	Sequence 4, Appli	Sequence 381, App	Sequence 384, App	Sequence 27, Appl	Sequence 44, Appl	
аг	US-09-757-415A-3	US-09-805-020-47	US-10-307-817-6	US-09-925-302-714	US-09-925-302-714	US-10-302-812-42	US-09-757-415A-2	US-10-307-817-8	US-10-204-041-2	US-10-394-322A-26	US-10-307-817-4	US-10-087-192-381	.US-10-087-192-384	US-10-394-322A-27	US-10-302-812-44	
	10	12	12	0	12	16	10	12	14	15	12	12	12	15	16	
Query Match Length DB	. 22	702	735	764	764	820	822	822	822	822	824	451	609	821	821	
Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	94.4	94.4	77.6	77.6	
Score	107	107	107	107	107	107	107	107	107	107	107	101	101	83	83	
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Sequence 254, App Sequence 1134, App Sequence 1267, App Sequence 366, App Sequence 366, App Sequence 227789, Sequence 227789, Sequence 718, App Sequence 110884, Sequence 115841, Sequence 115841, Sequence 115841, Sequence 115841, Sequence 115841, Sequence 115841, Sequence 115841, Sequence 115841, Sequence 115841, Sequence 115841, Sequence 115841, Sequence 115841, Sequence 116476, App Sequence 116476, App Sequence 116476, App Sequence 116476, App Sequence 116476, App Sequence 116476, App Sequence 116476, App Sequence 116476, App Sequence 116476, App Sequence 116476, App Sequence 118289, App S	edneuc edneuc edneuc edneuc
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ALIGNMENTS

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APPLICANT: Zhou, Ming-Ming
TITLE OF INVENTION: Methods of Identifying Modulators of the FGF Receptor
FILE REFERENCE: 25591-0007
CURRENT FILING DATE: 2001-01-09
PRIOR PAPLICATION NUMBER: 06/175967
PRIOR PLING DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 22
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100.0%; Pred. No. 4.9e-11;
iive 0; Mismatches 0;
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                                   Sequence 3, Application US/09757415A ; Publication No. US20030040612A1 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    22; Conservative
                                                                                                                                                                                                                                                                                                               TYPE: PRT
CRGANISM: Mus musculus
US-09-757-415A-3
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Best Local Similarity
Matches 22; Conserv
RESULT 1
US-09-757-415A-3
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1 HSQMAVHKLAKSIPLRRQVTVS 22

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APPLICANT: LEVINE, Zurit TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES FILE REFERENCE: 2786-0168P CURRENT APPLICATION UNMEER: US/09/805,020 US-09-805-020-47
; Sequence 47, Application US/09805020
; Publication No. US20020086384A1
; GENERAL INFORMATION:

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TYPE: PRT
ORGANISM: HOMO
FEATURE:
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LOCATION: (81)
      LOCATION: (81)
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NAME/KEY: SITE
NAME/KEY: SITE
OCHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/10307817
Publication No. US20040058338A1
GENERAL INFORMATION:
APPLICANT: Agee et al TITLE OF INVENTION:
NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE REPERENCE: 21402-502C
CURRENT APPLICATION NUMBER: US/10/307,817
CURRENT FILING DATE: 2020-12-02
SOFTWARE: CLEASEQLIST Version 0.1
SEQ ID NO 6
LENGTH: 735
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| Sequence 714, Application US/09925302
| Patent No. US20020044941A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al. |
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PALO4
| CURRENT APPLICATION NUMBER: US/09/925,302
| CURRENT FILING DATE: 2001-08-10
| PRIOR APPLICATION NUMBER: PCT/US00/05918
| PRIOR APPLICATION NUMBER: 60/124,270
| PRIOR FILING DATE: 1999-03-12
| NUMBER OF SEO ID NOS: 896
| SOFTWARE: Patentin Ver. 2.0
| SEO ID NO 714
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100.0%; Score 107; DB 12;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
Matches 22; Conservative 0; Mismatches 0;
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CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 47
LENGTH: 702
TYPE: PRT
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-805-020-47
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ORGANISM: Homo sapiens
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US-10-307-817-6
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids MAME/KEY: SITE LOCATION: (125) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids LOCATION: SITE LOCATION: (725) OTHER INFORMATION: Aaa equals any of the naturally occurring L-amino acids OTHER INFORMATION: Aaa equals any of the naturally occurring L-amino acids
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LOCATION: (44)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (62)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
OTHER INFORMATION: deliber and acids
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LOCATION: (125)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Publication No. US20040087016A1
GENERAL INFORMATION
APPLICANT: Keating et al.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CELL DEDIFFERENTIATION AND
                                                                                                                                                                                                                                                                                                                                         Gaps
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100.0%; Score 107; DB 9; Length 764;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels C
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APPLICANT: ROSE = al.
APPLICANT: ROSE = al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies;
FILE REPERENCE: PAl04
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR PLING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOPTHARE: Patentin Ver: 2.0
SEQ ID NO 714
LENGTH: 764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          351 HSQMAVHKLAKSIPLRRQVTVS 372
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                                                                                                                                                                                                                                                                                                                                                                                                      1 HSOMAVHKLAKSIPLRROVTVS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
US-09-925-302-714
; Sequence 714, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
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409 HSQMAVHKLAKSIPLRRQVTVS 430
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US-10-394-322A-26
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Publication No. US20030040612A1
GENERAL INFORMATION
OF US20030040612A1
GENERAL INFORMATION
TITLE OF INVENTION: Methods of Identifying Modulators of the FGF Receptor
FILE REFRENCE: 2459-1-002N
CURRENT APPLICATION NUMBER: 60/175867
PRIOR APPLICATION NUMBER: 60/175867
PRIOR FILING DATE: 2000-01-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3:1
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Publication No. US20040058338A1
GENERAL INFORMATION:
APPLICANT: Agee et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE REPERRENCE: 21402-502C
CURRENT APPLICATION NUMBER: US/10/307,817
CURRENT FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 68
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100.0%; Score 107; DB 12; Length 822;
Best Local Similarity 100.0%; Pred. No. 3e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0;
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Best Local Similarity 100.0%; Pred. No. 3e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 107; DB 10; Length 822; 100.0%; Pred. No. 3e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
TITLE OF INVENTION: TISSUE REGENERATION FILE REFERENCE: HYDR-P02-004 CURRENT APPLICATION NUMBER: US/10/302,812 CURRENT FILING DATE: 2002-11-21 NUMBER OF SEQ ID NOS: 78 SOFTWARE: Patentin version 3:1 SEQ ID NO 42 LENGTH: 820
                                                                                                                                                                                                                                                                                                                                                                                   407 HSQMAVHKLAKSIPLRRQVTVS 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  409 HSQMAVHKLAKSIPLRRQVTVS 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22; Conservative
                                                                                                                                                                         TYPE: PRT
CRGANISM: Homo sapiens
US-10-302-812-42
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ORGANISM: Homo sapiens
US-10-307-817-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-757-415A-2
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LENGTH: 822
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APPLICANT: SALASSIDES, KONSTADINOS
APPLICANT: SALASSIDES, KONSTADINOS
APPLICANT: BACHER, GERALD
APPLICANT: BACHER, GERALD
APPLICANT: MILLER, STEFAN
TITLE OF INVENTION: Pyridylpyrimidine Derivatives as Effective Compounds Against Prior
TITLE OF INVENTION: Infections and Prion Diseases
FILE REFERENCE: AXM-007.1P US
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: EP 01111858.5
PRIOR APPLICATION NUMBER: PCT/EP02/05420
PRIOR APPLICATION NUMBER: PCT/EP02/05420
PRIOR PILING DATE: 2002-05-16
NUMBER OF SEQ ID NOS: 20
SOFTWARF: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 822
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100.0%; Pred. No. 3e-09;
tive 0; Mismatches 0; Indels 0;
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Sequence 26, Application US/10394322A

Publication No. US20030232391A1

GENERAL INFORMATION:
APPLICANT: SUBSESS PHARMACEUTICALS, INC.
APPLICANT: STRESS PHARMACEUTICATION OF KINASE INHIBITORS
FILE REFERENCE: 39750-0006 US
CURRENT APPLICATION NUMBER: US/10/394,322A

CURRENT APPLICATION NUMBER: US 60/366,892

PRIOR FILING DATE: 2002-03-21

NUMBER OF SEQ ID NOS: 70

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 26

LENGTH: 822
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Sequence 2, Application US/10204041
Publication No. US20030176443A1
GENERAL INFORMATION:
APPLICANT: STEIN-GERLACH, MATTHIAS
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Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT; ORGANISM: Homo sapiens
US-10-204-041-2
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Gaps

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Indels

Length 609;

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94.4%; Score 101; DB 12;
illarity 95.5%; Pred. No. 2.2e-08;
Conservative 0: Mismatch-1
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 384 LENGTH: 609
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ORGANISM: Homo sapiens
US-10-394-322A-27
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ORGANISM: Homo sapiens
US-10-302-812-44
                                                                                          ORGANISM: Homo sapiens
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Best Local Similarity
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US-10-302-812-44
                                                                    TYPE: PRT
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                        APPLICANT: Agee et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE REFERENCE: 21402-502C
CURRENT APPLICATION NUMBER: US/10/307,817
CURRENT FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 682
SOFTWARE: CuraSeqList version 0.1
LENGTH: 824
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94.4%; Score 101; DB 12; Length 451;
Best Local Similarity 95.5%; Pred. No. 1.6e-08;
Matches 21; Conservative 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mortis, David W.
APPLICANT: Engelhard, Eric K.
ITLEO PINVENTION: NOVELE COMPOSITIONS AND METHODS FOR
ITLE OF INVENTION: NOVELE COMPOSITIONS AND METHODS FOR
ITLE OF INVENTION: OCANCER
FILE REFERENCE: 529452000122
CURRENT FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: PREUSE (FILING DATE: 2010-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: REALSEQ for Windows Version 4.0
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APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER FILE REFERENCE: 529452000122; CURRENT APPLICATION NUMBER: US/10/087,192; CURRENT APPLICATION NUMBER: US/09/147,377; PRIOR FILING DATE: 2000-12-22; PRIOR FILING DATE: 2000-12-22; PRIOR FILING DATE: 2001-03-03; NUMBER FILING DATE: 2001-03-02; NUMBER OF SEQ ID NOS: 2059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    411 HSQMAVHKLAKSIPLRRQVTVS 432
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; Sequence 381, Application US/10087192

; Publication No. US20020182586A1

; GENERAL INFORMATION:
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Publication No. US20020182586A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-307-817-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CRGANISM: Mus musculus
US-10-087-192-381
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Best Local Similarity
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       GENERAL INFORMATION
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US-10-087-192-384
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CELL DEDIFFERENTIATION AND TITLE OF INVENTION: TISSUE REGENERATION
FILE REPERENCE: HYDR-PO2-004
CURRENT APPLICATION NUMBER: US/10/302, 812
CURRENT FILING DATE: 2002-11-21
NUMBER OF SEQ ID NOS: 78
SOSTWARE: PATENTIN VETSION 3.1
SEQ ID NO 44
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Pred. No. 3.7e-05;
0; Mismatches 3; Indels
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Pred. No. 3.7e-05;
                                                                                              US-10-394-322A-27

Sequence 27, Application US/10394322A

Sequence 27, Application US/2003023391A1

Publication No. US20030232391A1

Publication No. US20030232391A1

APPLICANT: SUNBSIS PHARMACEUTICALS, INC.

TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
FILE REPERBNCE: 39750-0006 US

CURRENT APPLICATION NUMBER: US/10/394,322A

CURRENT FILING DATE: 2003-03-20

PRIOR PILING DATE: 2003-03-21

NUMBER OF SEQ ID NOS: 70

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 27

LENGTH: 821
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586 HSQMAVHKLAKSIPLRRQVTES 607
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Best Local Similarity 85.7%;
Matches 18; Conservative C
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Best Local Similarity 85.73
Matches 18; Conservative
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Search completed: August 2, 2004, 09:40:46 Job time: 11.7237 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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HSFGFR
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HUMBFGFS
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HUMFGF1A
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Match 1
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-MODEL=frame+ p2n.model -DEV=x1h
-Q=/Cegn2 1/USPTO_spool/US09757415/runat_02082004_101230_6685/app_query.fasta_1.526
-Q=/Cegn2 1/USPTO_spool/US09757415/runat_02082004_101230_6685/app_query.fasta_1.526
-Q=/Cegn2 1/USPTO_spool/US09757415/runat_02082004_10-1-COOPCL=0_-LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=1 -MATRIX=DO00000000
-USER=US09757415_@CGN 1 1 3851_@runat_02082004_101230_6685 -NCPU=6 -ICPU=3
-NO MMAAP -LIARGEQUERY -NGG SCORES=0 -WAIT -DSPEDCOCK=100 -LONGLOG
-DEV TIMBOUT=120 -WARN TIMBOUT=30 -THEMADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                     8, 2004, 19:45:10 ; Search time 806.618 Seconds (without alignments) 1182.153 Million cell updates/sec
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                              OM protein - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1 HSQMAVHKLAKSIPLRRQVTVS 22
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Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext Delop 6.0 , Delext
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Jatabase

X51893 Mouse fms-1
X57121 Human mRNA
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AR019675 Sequence
X51803 Human mRNA
BC033447 Mus muscu
AF176552 Mus muscu
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AR880743 Sequence
X57122 Fuman mRNA
X57119 Fuman mRNA
A29216 H.sapians D
I66313 Sequence 1
AX481457 Sequence 1
D12498 Rat mRNA fo
M65053 Mouse fibro
BD165930 Antisense
U22324 Mus musculu
M28998 Mouse basic

M63889 Human hepar Y00665 Human flg (U23445 Mus musculu

ALIGNMENTS

BC053921 Mus muscu AR201617 Sequence M34186 Human Libro E03799 cDNA sequen BC010200 Mus muscu M60485 Human Libro X66945 H. sapiens N AX887712 Sequence BC018128 Homo sapi

Sequence Primer fo Homo sapi

AX883990 BD160651 BAX024388 F

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during endothelial cell differentiation
Oncogene 3, 9-15 (1988)
On Oct 18, 1994 this sequence version replaced gi:31427.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                     Codon_start=1
product="tyrosine kinase"
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clone_lib="lambda-gt11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSFLGNR 1974 bp mRNA linear PRI 28-JUL-1995
Human flg (fms-like gene) mRNA for putative protein tyrosine kinase
(partial).
                           HUMHBGFC 1608 bp mRNA linear PRI 27-APR-1993
Human heparin-binding growth factor receptor (HBGF-R-alpha-a3)
mRNA, complete cds.
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(Dases 1 to 1974)

Ruta,M., Howk,R., Toca,G., Drohan,W., Zabelshansky,M., Laureys,G., Barton,D.E., Francke,U., Schlessinger,J. and Givol,D. A novel protein tyrosine kinase gene whose expression is modulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1102 CACAGCCAGATGGCTGTGCACAAGCTGGCCAACAGCATCCCTTGCGACAACAGATAGA 1161
                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1608)
Hou, J.Z., Kan, M.K., McKeehan, K., McBride, G., Adams, P. and McKeehan, W.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 HisserGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
                                                                                                                                                                                                                                                                                 Physological growth factor receptors from liver vary in three structural domains
Science 251 (4994), 665-668 (1991)
                                                                                                                                                                                                                                                                                                                                                                                    source text: Homo sapiens liver cDNA to mRNA. Location/Qualifiers % \left( 1\right) =\left( 1\right) =\left( 1\right) 
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Conservative:
Mismatches:
Indels:
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Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
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gene="HBGF-R"
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Homo sapiens (human)
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MMVD3445 Mus musculus fibroblast growth factor receptor-1, short isoform precursor mRNA, complete cds.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mamanlai; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Muscases 1 to 2259)
Jin,Y., Pasumarthi,K.B., Bock,M.E., Lytras,A., Kardami,E. and
                                                                                                                                                                                                                                                                                                                            1 HisSerGlnMetalaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr
                                                                                                                            1974
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Matches:
Conservative:
Mismatches:
<1. .1866
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1174 GTGTCT 1179
                                    Unknown.
Unclassified.
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KRQTVVRADSCASKMGSVLIVRPRLSSSGTPRAGVSSTBLEDEPRWELPERRELVLG
KRLGEGCFGGOVLARPATIGLDKVRNYTKVAYKMLKDDATEKDLSDLISEMENKKMIG
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KEGHRMDKPSNCTNELLYMWREDCWHAVPSQRPTFKQLVEDLDRIVALTSSGEYLDLSI
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Cattini, P.A. Cattini, P.A. Cattini, P.A. Cattini, P.A. Cattini, P.A. Stock and expression of fibroblast growth factor receptor-1 isoforms in the mouse heart: evidence for isoform switching during heart development M. Mol. Cattini Cardiol. 26 (11), 1449-1459 (1994) 95205422 Cell. Cardiol. 26 (11), 1449-1459 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
                                                                                                          2 (bases 1 to 2259)
Jin,Y.
Direct Submission
Submitted (24-MAR-1995) Yan Jin, Physiology, University of
Manitoba, 730 William Avenue, Winnipeg, Manitoba R3E 307, Canada
Location/Qualiflers
1. .2259
                                                                                                                                                                                                                                                                                                                                 58. 72259
/note="FGFR-1(S); similar to mouse FGFR-1(L), Genbank
Accession Number U22324, but does not encode the first
immunoglobulin like domain of FGFR-1(L)"
                                                                                                                                                                                                                                                                                                                                                                                                'codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118. .2256
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                tissue type="heart"
'dev stage="embryo (15 days)"
88. 72559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
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/mol type="mRNA"
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                                                                                                                                                                                                                                                                     'db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="FGFR-1(S)"
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Best Local Similarity:
Query Match:
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LOCUS
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                                                              JOURNAL
MEDLINE
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TITLE
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1114 CACAGCCAGATGGCTGTGCACAAGCTGGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1173
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Fuman mRNA for fibroblast growth receptor 2-Ig domain.
X57122.
X7122.1 GI:31386
FGF receptor; fibroblast growth factor receptor; immunoglobulin
domain.
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1 (bases 1 to 2360)
Cocks, B.G., Stuart, S.G. and Seilhamer, J.J.
Compositions for the detection of blood cell and immunological response gene expression
Patent: US 6607879-A 1288 19-AUG-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 2360)
Tronick, S.R.
Submitted Submission
Submitted (02-JAM-1991) S.R. Tronick, NATIONAL INSTITUTES OF
HEALTH, NATIONAL CANCER INSTITUTE, BLDG 37/RM 1E24, BETHESDA
MARYLAND 208992, USA
See also X57118-X57122.
                                                                                                                                                                                                                                                      2360
222
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Matches:
Conservative:
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Indels:
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1180 GTGTCT 1185
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Best Local Similarity:
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SOURCE
ORGANISM
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AUTHORS
                                                     mRNA
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A29216
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Alternative splicing generates at least five different isoforms of
the human basic-FGF receptor
Chocogene 6 (7), 1195-1202 (1991)
91319400
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'product="Fibroblast Growth Factor Receptor, 2 Ig-Domain
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Homo sapiens
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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See also X57118-X57122.

L. 2366
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Matches:
Conservative:
Mismatches:
Indels:
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Tronick, S.R.
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TITLE
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TITLE
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HSFGR2IGA
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A29216 2469 bp DNA linear PAT 30-JUN-1995
H.sapiens DNA for bFGF receptor from patent WO9111459.
A29216
A29216.1 GI:1247528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Homo sapiens
Bukaryotas, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2469)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR FORM OF THE HUMAN FIBROBLAST GROWTH FACTOR RECEPTOR Patent: WO 9111459-A 11 08-AUG-1991; Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 HisserGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr
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Indels:
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/db_xref="GOA:P11362"
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Matches:
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                l. .2366
/evidence=experimental
dev_stage="embryo"
germline
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1 (Dases 1 to 2469)

Nova,M. Philip,, Gonzalez,A.-M. and Baird,A. Process for the detection of malignant melanoma Patent: US 5670323-A 1 23-SEP-1997;
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Sequence 1 from patent US 5670323.
166313.1 GI:2724290
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1 (bases 1 to 2469)
Yazaki,N., Hiroko,P., Mitsuhiro,O., Toshisuke,K. and Nobuyuki,I.
The structure and expression of the FGF receptor-1 mRNA isoforms in
rat tissues
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   PAT 16-AUG-2002
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Submitted (26-UUN-1992) Itoh Nobuyuki, Kyoto University Faculty of
Pharmaceutical Sciences, Department of Biological Chemistry;
Sakyo-ku, Kyoto, Kyoto 606-01, Japan (Tel:81-75-753-4562,
Pax:81-75-761-8949)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                Kreutzer, R., Limmer, S., Rost, S. and Hadwiger, P. Method for inhibiting the expression of a target gene Patent: WO 02055693-A 71 18-JUL-2002; Ribophara AG (DE)
   linear
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2 (bases 1 to 2469)
Nobuyuki,1.
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Mismatches:
   DNA
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Matches:

    2469
    /organism="Homo sapiens"
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 AX481457 2469 bp 1
Sequence 71 from Patent WO02055693.
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                                    /organism="Mus musculus"
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/db Xref="taxon:10090"
/cell_line="FGF-responsiveSC-3"
/tissue type="breast cancer"
/ gene="FGF"
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JP 2001252085-A/5.
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/gene="FGF"
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NAPSGCSPITY FSVINVSDALESSEDDDDDDSSSEEKETDNYKRNRPVAPYWTSPEK
MEKKLHAVPAAKTVKFKCPSSGTPSPILRMLKNUGKEFKDPHRIGSYKYRATWSIIMD
SVVPSDKGNYTCIPARSGSTSINHTYQLDVVBRSPHRPILQAGLPANKTVALGSNVER
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/grotein_id="man02059.1"
/db_xref="G1:220738"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAGEYTCLAGNSIGLSHHSAWLTVLEALEERFÄWMTSPLYLEIIIYCTGAFLISCMVG
SVIIYKMKSGTKKSDFHSQMAVHKLAKSIPLRRQVTVSADSSASMNSGYLLVREBELS
SSGTPMLAGVSEYELPEDPRWELPRDRLVLGKPLGEGGFGQVVLAEAIGLDKDKPNRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKVAVYMLKEDATEKOLSDIJSEMEYMKMIGKHKNIINLLGACTQDGFLYVIVEYASK
GNLREYLQARRPPGLEYCYNPSHNPEEQLSSKOLVSCAYQVARGMEYLASKKCIHRDI
AARNVLVTEDNVMKIADPGLARDIHHIDYYKKTTNGRLPVKMMAPEALFDRIYTHQSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VWSFGVLLWEIFTLGGSPNPGVPVEELFKLLKEGHRMDKPSNCTNELYMMARDCWNAV
PSGRPTFKQLVEDLDRIVALTSNQEYLDLSMPLDQDSPSFPDTRSSTCSSGEDSVFSH
BPFPEEPCLPRHPTQLANGGLNRR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Original source text: Mouse FGF-responsive breast cancer cell line SC-3, cDNA to mRNA.

Location/Qualifiers
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Mouse fibroblast growth factor mRNA, complete cds.
M65053
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Matches:
Conservative:
Mismatches:
Indels:
   1. .2469
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Wister"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61. .2466
/product="FGF receptor-1"
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                                                                                                              /db xref="taxon:10116"
/sex="male"
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                                                                                                                                                                     /tissue_type="brain"
/dev_stage="adult"
1...2469
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fibroblast growth factor.
Mus musculus (house mouse)
Mus musculus
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TCB 1 (bases 1 to 2526)

Matsuda,Y., Tanaka,Y., Takeuchi,H. and Uchida,K.

Antisense nucleic acid compound

Antisense nucleic acid compound

Patent: UP 2001252085-A 5 18-SEP-2001;

TOA GOSEI CC LTD

PN JP 2001252085-A/5

PD 18-SEP-2001

PF 15-MAR-2000 UP 200072741

PI YOKO MATSUDA,YOICHI TANAKA,HIROAKI TAKEUCHI,KIYOSHI UCHIDA PC
C12N15/09,A61K31/711,A61K48/00,A61P43/00,C12N15/00 CC
Strandedness: Single,
CC Topology: Linear;
FH Key

LOCATION/Ohalifiorn
                                                                                                                                                                                                                                 1255 CATAGCCAGATGGCTGTGCACAAGCTGGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1314
                                                                                                                                                                                                                                                                                                                                                                                                                                       linear PAT 27-AUG-2002
                                                                                                                                                                                                 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr
Length:
Matches:
Conservative:
Mismatches:
Indels:
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DAGEYTCLAGASIGLSH4SAWLTVLEALEERAAWTSPLYLEIIIYCTGAFLISCMLG
SVITYKOMKSGTWKSDFHSQNAVHKLAKSIFLRRQYTVSADSSASMASGVLLVRPSRLS
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SVITYRATAGLKSDFHSPRELPEDRLYLGKPLGGGGCFQQVVLAEAIGLDKDKPNRV
TKVAYNGLKSDATBEDLSEBERMKMTGKHNIINLGACTQOGSPLYTIVBYASK
GNLREYLQARRPPGLEYCYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKKCIHRDL
WASRVLLWEINVWKLADFGLARDIHHIDYYKKTTNGRLPWKMAPPALLFDRIYHQSD
VWSFGVLLWEITTGGSPYPGVPVEELFKLLKEGHRMDKFSNCTNELYMMMRDCWHAV
PSQRPFFKQLVBDLARSYVALTSSQFEDFLSIELFKLLKEGHRMDKFSNCTNELYMMRDCWHAV
PSQRPFFKQLVBDLARSGLKRR"
CKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNTTDKEMEVLHLRNVSFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1282 CATACCGAGATGGCTGTGCACAAGCTGGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse basic fibroblast growth factor receptor (bFGF-R) mRNA, complete cds.
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Location/Qualifiers
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Reid, H.H., Wilks, A.F. and Bernard, O.
Two forms of the basic fibroblast growth factor receptor-like mRNA are expressed in the developing mouse brain Proc. Natl. Acad. Sci. U.S.A. 87 (4), 1596-1600 (1990)
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fibroblast growth factor receptor; transmembrane protein; tyrosine
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                                                                                                                                                                                                                                                                      148. .414
/note="encodes the first immunoglobulin like domain whic
is absent in FGFR1(S), Genbank Accession Number U23445"
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                                                                                                                                                                                                                                                                                                                              499. .504
/note="miniexon present in 1 out of 4 of our FGFR1(L)
clones"
                                                                                                                                                                                          118. 2523
/product="fibroblast growth factor receptor-1, long
isoform"
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/codon_start=1
/protein_id="AAA37290.1"
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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
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Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus fibroblast growth factor receptor-1 mRNA, long isoform precursor, complete cds.
U22324.1 G1:722340
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                                                                                                                                                                                                                                                                                                         Cloning and expression of fibroblast growth factor receptor-1 isoforms in the mouse heart: evidence for isoform switching during heart development
J. Mol. Cell. Cardiol. 26 (11), 1449-1459 (1994)
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Jin. Y., Pasumarthi, K.B., Bock, M.E., Lytras, A., Kardami, E. and Cattini, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="fibroblast growth factor receptor-1, long
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Direct Submission
Direct Submission
Submitted (06-MAR-1995) Yan Jin, Physiology, University of
Submittoba, 730 William Avenue, Winnipeg, Manitoba R3E 3J7, C
Location/Qualifiers
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/db_xref="G1:722341"
                  /organism="unidentified"
/mol_type="genomic RNA"
/db_xref="taxon:32644"
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Mus musculus
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Search completed: August
Job time : 814.618 secs
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Mouse fms-like gene (mflg) mRNA for fibroblast growth factor
X51893
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Safran,A., Avivi,A., Orr-Urtereger,A., Neufeld,G., Lonai,P., The murine fly gene encodes a receptor for fibroblast growth factor Oncogene 5 (5), 635-643 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1282 CATAGCCAGATGGCTGTGCACACAGTGGCCAAGAGCATCCCTCTGCGCCAGACAGTAACA 1341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58. 117
/note="fibroblast growth factor-receptor signal peptide
(put.); putative"
118. .2523
/product="fibroblast growth factor-receptor"
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Direct Submission
Submitted (20-FBB-1990) Safran A.,
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/mol_type="mXNA"
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/tissue_type="brain"
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Location/Qualifiers
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ORGANISM
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VERSION
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TITLE
JOURNAL
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AUTHORS
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MMFGF
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                                                                                                                                                                                                                                                                                                                                                                          GEYTCLAGN I GLSHHSAWLTVLEALEERPÄVMTSPLYLEI I I YCTGAFLI SCMLGSV
I I YKMKSGTKKSDPHSQMAVHKLAKS I PLRRQVTVSADSSASNNSAVLLVRPSRLSSS
GTPMLAGVSEYELPEDPRWELPRDKLVLGKPLGEGGFGQVVLAEAI GLDKDKPNRVTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAVXALKSDATEKDLSDLISEMEMMKMIGKHKNIINLLGACTODGPLYVIVEYASKGN
LREYLQARRPPGLEYCYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKKCIHRDLAA
RNVLVTEDNVMKIADFGLARDIHHIDYYKKTTNGRLPVKMMAPEALFDRIYTHQSDVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFGYLLWELFTLGGSPYPGVPVEELFKLLKEGHRMDKPSNCTYELYMMMRDCWHAVPS
QRPTFKQLVEDLDRIVALTSNQEYLDLSIPLDQYSPSFPDTRSSTCSSGEDSVFSHEP
LPEEPCLPRHPTQLANSGLKRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184. .2580
/product="fibroblast growth factor receptor (AA 1 to 799)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr
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/db_xref="GOA:116092"
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Conservative:
Mismatches:
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clone lib="lambda gt11"
21. .2583
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Human rep Human tes Human tes Human edu Rat seque Clone pra Human ect KGF recep Human FGF Human FGF

Farnesyl Fibroblas Human cDN Mouse bFG N-sam cDN

Lung canc Breast ca cDNA enco Human cDN

Human pol Clone pTB bek recep

Lung canc Kidney ca Fibroblas Bek-like Keratinoc

Perfect score:

Sequence:

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Scoring table:

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Abv78201 Abv78201 Abz35777 Abz35777 Abs11742 Abs116850 Abs166289 Abl66289 Abl66589 Abv19076
                                                                                                                                                                                                                                                                                                                                                                                                             Basic fibroblast growth factor; human; ss.
                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                              ABV78201
ABZ35777
ABX10020
                                                                                                                                        ACH17485
ABK63559
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1. 2469
1. 1469
1. 153
4. 1466
4. 12466
4. 1469
              AAQ10448
AAQ20914
                                                                                                   AAH18659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FARM ) FARMITALIA ERBA SRL CARLO.
                                                                                                                                                                                                                                                                                                                                         AAQ13311 standard; cDNA; 2469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90GB-00001466
                                                                                                                                                                                                                                                                                                                                                                       (revised)
(first entry)
Basic FGF receptor.
23-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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28-OCT-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sig_peptide
AAQ13311;
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Command line parameters:
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-MODEL=frame+ pan.model -DEV=xlh
-MODEL=frame+ pan.model -DEV=xlh
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-LIST=45 -DOCALIGN=200 -THR_SCORE=pape1XEX=500 -MINLEN=0 -MAXLEN=200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aaq13311 Basic FGF
Abv78187 Human FGF
Abx10006 Human FGF
Ab101728 Human pol
Aba01689 Mouse fib
Aaq21089 flg recep
Aad52780 Human FGF
                                                    2004, 19:43:05 ; Search time 86.8421 Seconds (without alignments) 1076.210 Million cell updates/sec
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        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                       nucleic search, using frame_plus_p2n model
                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                  3373863 segs, 2124099041 residues
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Maximum Match 100%
Listing first 45 summaries
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ABV78187
ABZ35763
ABX10006
ABL91728
ABAQ1689
AAQ21003
                                                                                             107
1 HSQMAVHKLAKSIPLRRQVTVS
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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geneseqn2001as:*
geneseqn2001bs:*
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geneseqn1990s:*
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Maximum DB seq length: 200000000
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Match 1
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Database :

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12 M 4 M 9 F 8

Score

Result

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Sarmientos

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1225 CACAGCCAGATGGCTGTGCACAAGCTGGCCAAGAGCATCCCTCTGCGCAACAGGTAACA 1284
                                                                                                                                                              The sequence was obtd. from two overlapping clones, PL5 and PL10, isolated from a placental lambda gtil cDNA library. The DNA can be used to express recombinant bFGF receptor which is an antagonist of human aFGF and bFGF. The receptor can be used to treat abnormal angiogenesis (e.g. in diabetic retinopathy, neovascular glaucoma, etc., and possibly certain solid tumours), and in contraceptives. Dossage is 10.100 ug. See also AAQ13308-Q13311. (Updated on 25-MAR-2003 to correct PA field.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA inhibition; dsRNA1; gene expression inhibitor; oncogene; cytostatic; virucide; protozoacide; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                          HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr
                                                                             Extracellular form of human fibroblast growth factor receptor treat tumours, abnormal angiogenesis e.g. diabetic retinopathy, rheumatoid arthritis and arteriosclerosis and as contraceptives
                                                                                                                                                                                                                                                                          Sequence 2469 BP; 576 A; 712 C; 698 G; 483 T; 0 U; 0 Other;
             Roncucci R,
                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
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             Isacchi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABV78187 standard; DNA; 2469 BP.
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                                                                                                                                     Claim 3; Fig 2; 29pp; English.
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26-077-2001; 2001DE-01055280.
29-NOV-2001; 2001DE-01058411.
07-DEC-2001; 2001DE-01060151.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-NOV-2002 (first entry)
             Mazue G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Limmer S,
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                                       WPI; 1991-252611/34.
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Best Local Similarity:
                                                    P-PSDB; AAR13549
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             Bérgonzoni L,
                                                                                                                                                                                                                                                                                                      Alignment Scores:
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Inhibiting expression of target gene, useful e.g. for inhibiting

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Inhibiting expression of target genes, useful e.g. for treating tumors, by introducing into cells two double-stranded RNAs that are complementary to the target.
                                                                         The invention relates to inhibiting expression of a target gene (1) in a cell by introducing an inhibitory RNA (dsRNA1) having a double-stranded structure of at most 49 consecutive bases. At least part of one strand (as1) of dsRNA1 is complementary to (1) and at least part of one strand has an overhang of 1-4 nucleotides. The method is used to inhibit the expression of a wide range of genes, e.g. oncogenes, cytokine genes etc. in humans, also genes in Plasmodium or in viruses or viroids that are pathogenic for humans, animals or plants. Introducing an overhang into both in vivo and in vitro and also increases stability and thus the effective concentration inside the cell. The present sequence is that of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide; protocoacide; gene expression; antisense; tumour; infection; Plasmodium; virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus; Hepatitis C virus; human papilloma virus; gene; ds.
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oncogenes, by administering double-stranded RNA complementary target and having an overhang.
                                                                                                                                                                                                                                                                                      Sequence 2469 BP; 576 A; 712 C; 698 G; 483 T; 0 U; 0 Other;
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Matches:
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                                            Claim 10; Page 150-151; 203pp; German
                                                                                                                                                                                                                                                        a gene related to the invention
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                  The invention relates to inhibiting expression of a target gene in a cell by incroducing at least two oligoribonuclectides (daRNAI and II), both with a double-stranded (ds) structured at most 49 sequential nucleotide pairs. At least part of one strand (S1, S2) of the ds structures in each of dsRNAI and II are complementary to regions in the target gene. The method uses antisense inhibition of gene expression using double stranded RNA inhibition (RNAI). The method is particularly used to treat tumours or infections, especially by Plasmodium or viruses/viroids (pathogenic on humans, animals or plants). The method provides more effective inhibition of expression than known methods using a single dsRNA, even at very low concentrations. When dsRNA has at least one unpaired nucleotide at the concentration of and thus effective concentration in the cell) is improved and efficiency can be increased further by precreating the cells with interferon. The present sequence is that of a target DNA of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting expression of target genes, e.g. oncogenes, in cells, by introduction of complementary double-stranded oligoribonucleotide, after treating the cell with interferon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental;
prion; inhibition; human; ds.
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                                                                                                                                                                                                                                                                                                                                           1 HisSerGlnMetAlaValHisLysLeuAlalysSerIleProLeuArgArgGlnValThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 52; 98pp; German.
 Claim 13; Page 47; 100pp; German
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target gene by introducing into the cell that contains the target gene at least one oligoribonucleotide (dsRMI) that has a double-stranded (ds) structure of not more than 49 consecutive nucleotides (nt), where at least a segment of one strand of the ds structure is complementary with the target gene and the cells are treated with interferon before protein genes, particularly oncogens, cytokine genes, id (not defined) potein genes, particularly oncogens, cytokine genes, id (not defined) potein genes, particularly oncogens, cytokine genes expressed in pathogenic organisms (particularly plants). Treating the cells with interferor greatly increases the extent to which dsRNA on inhibit expression of the target genes, and the effect is even greater when dsRNA are modified to increase their stability, ABX09936-ABX10075 represent
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Plasmodium, virus, viroid, cytokine, prion, antisense oligonucleotide,
cytostatic, virucide, protozoacide, antibacterial, ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr
                                                                                                                                                                                                                                                                                                                                                                                                gene fragments used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2469 BP; 576 A; 712 C; 698 G; 483 T; 0 U; 0 Other;
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most 49 sequential nucleotide pairs, with at least part of one strand complementary. With the target game and has at least one on a single-stranded segment of 1-4 nt. The method provides oligoribonucleotides for antisense inhibition of gene expression useful e.g. for treating tumours but the oligoribonucleotides may also be directed against genes present in pathogens (e.g. plasmodium or viruses/viroids, pathogenic on humans, animals or plants) or against cytokine, Id, developmental or prion genes. The method provides more effective inhibition of gene expression than use of known oligonucleotides, probably because the unpaired overhang increases stability and thus intracellular concentration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1225 CACAGCCAGATGGCTGTGCACAAGGCTGGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes an antisense nucleic acid compound (I), used as a diagnostic and therapeutic agent. (I) comprises: (1) an antisense nucleic acid compound (II) having the base sequence TTGGTTT; (ii) an antisense nucleic acid compound (III) having the above base sequence in which the base number is expressed by a base sequence between 10 and 60; and (iii) an antisense nucleic acid molecule (IV) comprising one of the 3 sequences given in ABA01686 to AB01688, all comprising of 20 nucleic acids, and that inhibit the expression of fibroblast growth factor receptor 1 (FGFR1). (I) is useful as a treating agent, a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  growth factor receptor 1; FGFR1; antisense oligonucleotide;
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and a research reagent. The present sequence represent which is given in the exemplification of the present
                                                                                                                                                                                  1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr
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                                                                                                                                                                                                                                                                                                                                                                                                  Fibroblast growth factor receptor, heparin binding proteins, tyrosine kinase, fms-like gene, {\rm CSF-1}_1, {\rm PDGF}_1 ss.
                                             BP; 576 A; 710 C; 712 G; 0 T; 528 U; 0 Other;
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/note= "insertion; see comments"
1173. 1174
*tag= c/*tag= c/*tag= deletion; see comments"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schlessing J;
                                                                                                                                      Gaps:
                                                                                                                                                             US-09-757-415A-3 (1-22) x ABA01689 (1-2526)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
87. 2546
7. ttag= a
/product= "flg"
1105
                                                                                                                                                                                                                                                                                               AAQ21003 standard; cDNA; 2662 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jaye MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Fig 7; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (RORE ) RORER INT HOLDINGS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90US-00549587.
                                                                             7.78e-09
107.00
100.00$
100.00$
                                                                                                                                                                                                                                                                                                                                             (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                              Elg receptor protein gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Crumley G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             psoriasis, arthritis.
                                                                                                                                                                                                                                                   1342 GÜĞÜCA 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1992-056827/07.
P-PSDB; AAR20750.
                                                                                                                                                                                                                               21 ValSer 22
  diagnostic agent a
mouse FGFR1 mRNA,
                                                                                                     Percent Similarity:
Best Local Similarity:
                                              Sequence 2526
                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-1990;
                                                                    Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
20-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9200999-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dionne CA,
                          invention
                                                                                                                                                                                                                                                                                                                      AAQ21003;
                                                                                                                           Query Match:
                                                                                                                                                                                                                                                                           RESULT
  8X888
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compared (Ruta et al., Oncogene, 3: 9-15). A full length flg cDNA clone was obtd. by repeated rounds of PCR using 8 primers (AAQ23610-17), and was cloned into pMA30. NIH 3T3 cells were cotrarsfected with a 1:20 mixture of pSy2neo and an flg expression vector contg. the flg probe inserted into pMA30 immediately downstream of the SV40 promotor and contained into pMA30 immediately downstream of the SV40 promotor and contained for aFGP receptors, the best being clone Nfig26 which was used binding for aFGP receptors, the best being clone Nfig26 which was used for DNA sequencing. The sequence shown contains an apparent insertion case features) which disrupts the reading frame. This is restored, chowever, by a deletion downstream in the sequence. No reference is made by the authors to these discrepancies, which are therefore assumed to be compared an endomediate contains an apparent insertion contains an apparent in the sequence may be compourturistic pathogen to human cells. Such undesirable heparin-binding of growth factor mediated cellular responses or to inhibit the binding of an opportunistic pathogen to human cells. Such undesirable responses may be grown factor stimulated angiogene is and vascularisation of tumours, contenting protein may also be used for correcting drugs for treatment of such problems. See also AAQ21004.
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Sequence 2662 BP; 613 A; 787 C; 740 G; 522 T; 0 U; 0 Other;

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Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                        Gaps:
       8.316-09
107.00
100.00%
100.00%
                                    Similarity:
                           Percent Similarity:
Alignment Scores:
                                             Query Match:
DB:
                                      Best Local
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US-09-757-415A-3 (1-22) x AAQ21003 (1-2662)

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1312 CACAGCCAGATGGCTGTGCACAAGCTGGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1371
1 HisSerGlnMetAlavalHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
                                                                           1372 GTGTCT 1377
                                                           Valser 22
                                                             21
                               g
    ð
                                                             ò
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AAD52780 standard; DNA; 2662 AAD52780 RESULT

BP.

(first entry) 14-MAY-2003 AAD52780;

Human FGF-R1 DNA.

Human; pyridylpyrimidine derivative; cellular protein kinase; Scrapie; cellular protein phosphatase; cellular signal transduction; prophylaxis; prion infection; chronic wasting disease; CMD; Creuzzfeldt-Jacob disease; CUD; transmissible mink encephalopathy; bovine spongiform encephalopathy; TME; BSE; Gerstmann-Girauseler-Scheinker syndrome; GSS; Alpers syndrome; fatal familial insomnia; FFI; kuru; neurodegenerative disease; nootropic; Alzheimer's disease; FGF-R1; flg; F1-1; F1t-2; b-FGFR; gene; ds.

Homo sapiens

```
"Human FGF-R1 protein"
location/Qualifiers
              88. .2556
/*tag= a
/product= '
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WO200293164-A2

21-NOV-2002.

16-MAY-2002; 2002WO-EP005420

16-MAY-2001; 2001EP-00111858

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29-MAY-2001; 2001US-0293528P.
13-JUL-2001; 2001EP-00117113.
18-JUL-2001; 2001US-0305898P.
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₽Ġ. (AXXI-) AXXIMA PHARM Ω ., Mueller Bacher G, Salassidis K, Stein-Gerlach M,

WPI; 2003-120714/11.

New pyridylpyrimidine derivatives useful in the treatment or prevention of infectious disease e.g. Kuru syndrome and Creutzfeld-Jacob disease (CDD). P-PSDB; AAE34488

Disclosure; Page 61-62; 96pp; English.

The invention relates to novel pyridylpyrimidine derivatives and methods of detecting prion infections and/or prion disease in an individual or in cells. Cells intures and/or cell lysates. The method involves adding at least one monoclonal or polyclonal antibody, oligonuclectide or pyridylpyrimidine derivative to the sample or in cells, cell cultures and/or cell lysates and detecting the activity of at least one human cellular protein kinases (e.g., FGF-R1 (also known as flg, R1-1, P1L-2, b-FGFR), cell lysates and detecting the activity of at least one human cellular protein kinases (e.g., FGF-R1 (also known as flg, R1-1, P1L-2, b-FGFR), ce whown as CCK-2, DDR-2 or EDDR, EC number 2.7.1.112), Abl (also known as CDK1), PRX, human cellular protein phosphatases such as PTP-SL (also known as MCP83) and PTP-zeta, the cellular signal transduction conduction of prions in cells and in the manufacture of pharmaceutical production of prions in cells and in the manufacture of pharmaceutical composition for prophylaxis and/or treatment of infectious disease (e.g., composition wasting disease (CMD), bovine spongiform encephalopathy (TMB), creutifeldt-Jacob disease (CMD), bovine spongiform encephalopathy (TMB), variant CJD, Gerstmann-Straussler-Schennker syndrome (GSS), fatal familial insomnia (FFI), kuru and Alpers syndrome, especially BSE, CJD, contraction of the present sequence is human FGF-RI DNA used in the

Sequence 2662 BP; 613 A; 787 C; 740 G; 522 T; 0 U; 0 Other;

invention

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2662
22
0
0
0
     Length:
Matches:
Conservative:
Mismatches:
                                     Indels:
     8.316-09
107.00
100.00%
100.00%
                              Best Local Similarity:
                       Percent Similarity:
Alignment Scores:
                                      Query Match:
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US-09-757-415A-3 (1-22) x AAD52780 (1-2662)

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AAT31051 standard; DNA; 2733 GIGICT 1377 1372

Valser 22

21

8

26-FEB-1997 (first entry)

AAT31051;

Human fibroblast growth factor receptor; FGFR1; alpha exon; pre-mRNA; antisense oligonuclectide; inhibition; anti-tumour; glioma; glioblastoma; Human fibroblast growth factor receptor 1 gene

exon

```
1342 CACAGCCAGATGGCTGTGCACAAGCTGGCCAAGAGCATCCCTCTGCGCAGACACACATAACA 1401
                                                                                                                                                                                                                                                                                                                                                                               Composition useful for identifying modulators of fibroblast growth factor -mediated signaling for use in treating cancer, has ternary complex of FGF-receptor, FGF ligand and heparin agonist or antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to an isolated composition comprising a ternary complex of an Fibroblast Growth Factor (FGF) ligand polypeptide (ABR56163, ABR56163, an FGF receptor polypeptide (ABR56164) and a heparin agonist or antagonist, where the agonist or antagonist binds to the FGF receptor polypeptide to form the ternary complex. The composition is useful for identifying a compound that is an inhibitor of FGF receptor activity. FGF1 is also known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 623 A; 810 C; 765 G; 533 T; 0 U; 2 Other;
                                                118. .2586
/ttag=
/product= "FGFR1"
/transl_except= (pos:2566. .2568,aa:Gly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
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Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (1-2733)
                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 2B; 288pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQ10448 standard; cDNA; 2856 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-757-415A-3 (1-22) x ACC42967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human basic fibroblast growth
                                                                                                                                                                                                 31-OCT-2002; 2002WO-US034986.
                                                                                                                                                                                                                                  31-OCT-2001; 2001US-0335583P.
                                                                                                                                                                                                                                                                                                Linhard
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107.00
100.00%
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(first entry)
                                                                                                                                                                                                                                                                                                Green DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          drdrcr 1407
                                                                                                                                                                                                                                                                                                                                WPI; 2003-482144/45
P-PSDB; ABR56165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 ValSer 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity:
                                                                                                                                WO2003038054-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2733
   Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                 08-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
17-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acidic FGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1402
                                                                                                                                                                                                                                                                                                Moosa M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ10448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local
                                 Key
 1342 CACAGCCAGATGGCTGTGCACAAGGCTGGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antisense oligomers which hybridise to the human fibroblast growth factor receptor I pre-mRNA and inhibit FGFR1 expression are claimed. The oligomers pref. hybridise to the alpha-exon region and are useful for preventing growth of tumours, esp. glioma or glioblastoma cells. The present sequence is that of the FGFR1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inhibiting growth of tumour cells - using an anti:sense oligomer for the human fibroblast growth factor receptor-1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr
                                                                                                                                                              /*tag= a
/label= alpha
/note= "antisense oligomers pref. hybridise to this
                                                                *tag= b
note= "identity of nucleotide is provisional"
                                                                                                               "*tag= c
note= "identity of nucleotide is provisional"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2733 BP; 623 A; 811 C; 765 G; 532 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 54-55; 71pp; English
                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                Brown BD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACC42967 standard; DNA; 2733 BP.
                                                                                                                                                                                                                                                                                                              96WO-US000331
                                                                                                                                                                                                                                                                                                                                             95US-00371001
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100.00%
100.00%
                                                                                                                                              110. .467
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                                                                                                                                                                                                                                                                                                                                                                                                              Tseng BY,
                                                                                                                                                                                                              region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIGICT 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1996-342063/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 ValSer 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                             misc_difference
                                                                                             misc_difference
                                                                                                                                                                                                                                                                                                                                                                             (GENT-) GENTA
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                              Morrison RS,
                                                                                                                                                                                                                                                                                                                                             10-JAN-1995;
                                                                                                                                                                                                                                                WO9621471-A1
                                                                                                                                                                                                                                                                                                              11-JAN-1996;
                                                                                                                                                                                                                                                                             18-JUL-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-DEC-2003
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FGF; angiogenesis; neuron growth; ss.

Human Fibroblast Growth Factor Receptor 1 coding sequence.

ACC42967

ACC42967

Human; Fibroblast Growth Factor Receptor 1; FGFR1; protein co-ordinate data; gene; ds.

Homo sapiens

06-JUL-1989; 06-JUL-1989;

WO9100916-A

24 - JAN - 1991

sig_peptide mat_peptide

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The human basic fibroblast growth factor (b-FGF) receptor sequence was obtd. from a human placenta cDNA library in lambda gtll. The library was screened with two probes (AAQ24634,5) which were derived from the known FLG sequence (fms like gene). Positive clones were transformed into E. coli Y1090 strain, and recombinant phage were sequenced
                                                                                                                                                                                                                                                                                                                                                                                                                             Human b-FGF receptor gene - contains recombinant DNA, chromosome DNA or cDNA base sequence encoding polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, artery, endothelium, umbilical, vein, aorta, pulmonary artery, bronchial epithelium, prostate, muscle, lung fibroblast, osteoblast, tumour, microarray, genome mapping, antibiotic, antiviral, antifungal, gene expression, gene, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human gene expression profile polynucleotide SEQ ID NO 299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3328 BP; 777 A; 946 C; 902 G; 703 T; 0 U; 0 Other;
             Basic fibroblast growth factor; fms like gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
                                                                                                                                      /product
/note= "h bFGF receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
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                                                                                  ocation/Qualifiers
229. .2425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABZ35187 standard; cDNA; 3328 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 1; 10pp; Japanese.
                                                                                                                                                                                                                                                                                                                                          (MITK ) MITSUI TOATSU CHEM INC
                                                                                                                                                                                                                                                                     90JP-00141490.
                                                                                                                                                                                                                                                                                                     90JP-00141490.
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107.00
100.00%
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                                                                                                                          *tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ValSer 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAR21686
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                                                                                                                                                                                                JP04036184-A.
                                                                                                                                                                                                                                                                                                         10561-NDC-10
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                                                   Homo sapiens
                                                                                                                                                                                                                                                                     01-JUN-1990;
                                                                                                                                                                                                                                    06-FEB-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence was obtd. from a clone isolated from a huma ubilical vein endothelial cDNA library and a human placenta cDNA library using a probe can the hflg cDNA sequence. Four types of positive clones were isolated, divided into two classes based on their restriction patterns: based on the hflg cDNA sequence. Four types of positive clones were constant in the sequence of bases 2857 - 3612 appears to be absent from the consequence of bases 2857 - 3612 appears to be absent from the specification, with the 3' terminal of bases 3613-3636 given as: specification, with the 3' terminal of bases is growth factor complete which can be used for tissue repair or developement and for neuron maintainance. The DNA and protein and antibodies prepd. from it can be used to treat diseases resulting from aberrant RGF expression and for elucidating the mechanism of FGF and identify ing agonists for the prevention of angiogenesis and control of tumours. See also AAQ10448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1480 CACAGCCAGATGGCTGTGCACAGGCTGGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 HisSerGlnWetAlaValHisLysLeuAlalysSerlleProLeuArgArgGlnValThr 20
                                                                                                                                                                                                                                                                                                                                                                                                Fibroblast growth factor receptors - and clones encoding them, sol. fo
of receptors and antibodies to them useful for diagnostic studies and
therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2856 BP; 631 A; 872 C; 836 G; 517 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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 location/Qualifiers
                                                                                                                                                                                                                                                                                                               Lee PE;
                                                                          /*tag= b
/product= "bFGF-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 4; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ20914 standard; cDNA; 3328
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                                                                                                                                                                                                                                        89US-00377003.
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100.00%
100.00%
                                                     . .2721
                                                                                                                                                                                                                                                                                                             Williams LT, Johnson DE,
                                                                                                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA
                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1540 GTGTCT 1545
                                                                                                                                                                                                                                                                                                                                                  WPI; 1991-051340/07.
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAR10649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
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Alignment Scores:

03-JUL-1992

AAQ20914;

AAQ20914 ID AAQ2 XX AC AAQ2 XX DT 03-J XX DE Huma

RESULT 12

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farnesyl transferase inhibitor; gene expression;

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Determining whether a patient will respond to treatment with a farnesyl transferase inhibitor, by analyzing the expression of gene that is differentially modulated in the presence of the inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 98; 346pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
                                                    quinolinone; leukemia; cancer.
                                                                                                                                                                                                                                                                                                                            30-OCT-2001, 2001US-0338997D.
30-OCT-2001, 2001US-0340081P.
30-OCT-2001, 2001US-0340938P.
30-OCT-2001, 2001US-0341012P.
                                                                                                                                                                                                                                                                          30-OCT-2002; 2002WO-US034784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-513497/48.
                             ss; cytostatic;
                                                                                                                                                              WO2003038129-A2
                                                                                                            Homo sapiens.
                                                                                                                                                                                                                  08-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Raponi M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score:
The invention relates to a gene expression profile comprising one or more genes (AB2348894-AB235692) and generated from a cell type. The cell type is a coronary artery endothelium, umbilical artery or vein endothelium, acric endothelium, dermal microvascular endothelium, pulmonary artery endothelium, mammary epithelium, prostate epithelium, mornelial epithelium, mammary epithelium, prostate epithelium, renal cortical epithelium, artery smooth muscle, menal dermal fibroblast, pulmonary artery smooth muscle, menal dermal fibroblast, pulmonary artery smooth muscle, cortic smooth muscle, merangial cells, coronary artery smooth muscle, cortic smooth muscle, merangial cells, coronary artery smooth muscle, cortic smooth muscle, ung fibroblast, cortic smooth muscle, lung fibroblast, cortic smooth muscle, ung fibroblast, cortic smooth muscle, ung fibroblast, cortic smooth muscle, ung fibroblast, cortic smooth muscle, ung fibroblast, cortic smooth muscle, ung fibroblast, cortic smooth muscle, ung fibroblast, cortic smooth muscle, ung fibroblast, cortic smooth muscle, ung fibroblast, cortic smooth muscle, ung fibroblast, cortic smooth muscle, ung fibroblast, cortic smooth muscle, ung fibroblast, cortic smooth muscle, ung fibroblast, cortic smooth muscle, ung fibroblast, cortic smooth muscle, ung fibroblast, cortic smooth muscle, ung fibroblast, cortic smooth muscle, und distinguishing dell cypes. The gene or a procein cortic phenotype of a cell and distinguishing cell types. The gene or a procein cortic and profile is useful in identifying disease pathologies involving alternation with respect to tumour type and stage, treatment methods, and prognosis. The gene or protein expression profile cortic and physical mapping of genomes, DNA sequencing, genetic or dentifications and in identifying promising antibiotics, antiviral or antiviral or antiviral or antiviral or antiviral or antiviral or antiviral or
                                                                                                                                                                                                                                                                                                                                              New gene expression profile generated from primary, endothelial, epithelial, and muscle cell types, useful for identifying disease pathologies involving alterations of gene expression, e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3328 BP; 777 A; 946 C; 902 G; 703 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                            (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim.10; Page 454-455; 850pp; English
                                                                   20-MAR-2002; 2002WO-US008456
                                                                                                                        20-MAR-2001; 2001US-0276947P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.16-08
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Best Local Similarity:
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                                                                                                                                                                                                                                       Wan J, Wang Y;
                 26-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
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DB:
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1180 CACAGCCAGATGGCTGTGCACAAGCTGGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1239
The invention relates to a method of determining whether a patient will respond to treatment with a farnesyl transferase inhibitor (FTI), by analyzing the expression of gene that is differentially modulated in the presence of an FTI. The method is useful for determining whether a patient will respond to treatment with a FTI such as (B) 6-[amino 4-chlorophenyl) (1-methyl-1H-imidazol-5-tyl)methyl]-4-(3-chlorophenyl) 1-methyl-2-(1H)quinolinone, monitoring the therapy of a patient, treating a patient with leukemia with FTI if the analysis indicates that the patient will respond. This sequence of FTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZNF198-FGFR1; fibroblast growth factor receptor 1; oncogene; lymphoma; leukaemia; SCLL; translocation; stem cell; diagnosis; therapy; ss.
                                                                                                                                                                                                                                            BP; 777 A; 946 C; 902 G; 703 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                            3328
222
0
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                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-757-415A-3 (1-22) x ADE84879 (1-3328)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX87179 standard; cDNA; 3343
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                                                                                                                                                                                                                                                                                                                                                                          Similarity:
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                                                                                                                                                                                                                                            Sequence 3328
                                                                                                                                                                                                                                                                                     Alignment Scores:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
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1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr

US-09-757-415A-3 (1-22) x ABZ35187 (1-3328)

Farnesyl transferase inhibitor modulated leukemia associated gene #98

(first entry)

29-JAN-2004

ADE84879

ADE84879 ID ADE8 XX AC ADE8 XX DT 29-J XX DE Farn

ВР.

ADE84879 standard; DNA; 3328

1240 GrGrCr 1245 Valser 22

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RESULT 14

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Homo sapiens

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This is the nucleotide sequence of human fibroblast growth factor receptor 1 (FGFR1) cDNA. The FGRR1 gene is located on chromosome 8. A newly identified oncogene, SNF199-FGRR1 (see AAX87177), incorporates a CFRR1 tyrosine kinase domain fused through t (8,13) translocation to SNF198 a novel zinc finger gene of chromosome 13, and is associated with stem of the chromosome 13, and is associated with seem call letwisemia 4/ymphoma syndrome (SCLL) Molecular characterisation of the oncogene and the encoded oncoprotein (see AAY06456) provides the ability to identify patients with t (8;13) (p11;q11-12) syndrome prior to onset of mysociated on the demonstrate of mysolid leukaemia. The oncogene can be identified with primers and probes capable of hybridizing to ZNF198 or FGFR1 tyrosine kinase domain coding sequences. Cells containing ZNF198-FGFR1 can be located Attribodies that recognize this fusion juncture can also be used to deliver toxic substances to patients containing the ZNF198-FGFR1 protein. This is useful for treatment of SCLL. Antisense nucleotides and ribozymes targeted to ZNF198-FGFR1 nonceptine are useful for reducing expression or disrupting translation of the oncogene. (All claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Oncogene, designated ZNF198-FGFR1, useful in diagnosis of stem cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3343 BP; 766 A; 957 C; 911 G; 709 T; 0 U; 0 Other;
                                                                     /*tag= a
1287. .1288
/*tag= b
/note= "t(8,13) breakpoint"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 69-70; 76pp; English
                                 Location/Qualifiers
10. .2472
                                                                                                                                                                                                                                                                                                                  (BGHM ) BRIGHAM & WOMENS HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leukemia and lymphoma syndrome.
                                                                                                                                                                                                                                         99WO-US000365
                                                                                                                                                                                                                                                                               98US-00004688
                                                                                                                                                                                                                                                                                                                                                        Fletcher JA, Xiao S;
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-430381/36.
P-PSDB; AAY06458.
                                                                                                                                                                                                                                           07-JAN-1999;
                                                                                           misc_feature
                                                                                                                                                                  WO9935159-A1
                                                                                                                                                                                                                                                                               08-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                      15-JUL-1999.
                                     Key
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1228 CACAGCCAGAIGGCIGIGCACAAGCIGGCCAAAAGAGCAICCCTTGCGCAGAAGAAGAAAA 1287 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: US-09-757-415A-3 (1-22) x AAX87179 (1-3343) 1.11e-08 107.00 100.00% 100.00% Query Match: DB:

Percent Similarity: Best Local Similarity:

8, 2004, 21:31:41 Search completed: August Job time : 96.8421 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - nucleic search, using frame_plus_p2n model

August 8, 2004, 21:03:30 ; Search time 610.355 Seconds (without alignments) 1076.370 Million cell updates/sec 107 1 HSQMAVHKLAKSIPLRRQVTVS 22 US-09-757-415A-3 Title: Perfect score: Scoring table: Sequence: Run on:

0.07 BLOSUM62 Xgapp 10.0, Xgapext Ygapop 10.0, Ygapext Fgapop 6.0, Fgapext Delop 6.0, Delext

55026578 27513289 seqs, 14931090276 residues Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:
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-UB=EST -QFWT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=buman40.cdi -LIST=45
-UNITS=bits -START=1 -MATRIX=blosum62 -TRANS=buman40.cdi -LIST=45
-UNITS=bits -NORM=ext -HEAPSIZE=500 -WINLEN=0 -MAXIEN=200000000
-USER=US09757415_@CGN 1 1_4385_@runat_02082004_101231_6697 -NCPU=6 -ICPU=3
-NO MAAP -LARGEQUERS -NGG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=3 0 -THEABS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

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gb gss2:* 29: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	446321	X363360	262999	78197	772368	B706389	B800339	F922260	87182	38352	0624 99589	50008 B0305F05	95172 cs61b0	31255 60123107	7508 Vr32	7333 AU12733	928 mp16g07	897 AU12689	236 mm30009	8342 MR4	5564 UI-HF-	6112 2014-36	058 1 q 42b	4527 UI-M-FD	0452 dolybul	94753 MR3-UT0	F750302 UI-M-HJ0	F125642 UI-HF-EL	F868338 292100 B	I653629 60330027	113 502051	110/1509 / 5525	086/ UI-M-FD	1567 AULDISC	342 AUISUS4	40/6 AU1340/6	7084	5176 AGENCOUR	0700 AU130700	UBSS209 AGENCOU	1753909 60302291	119392 AU119392	0004 601768	1688445 60331638
B ID	D AW446	3 BY36336	3 BY36299	M70107	CR77036	CB7063	4 CB80033	0 BF92226	4 CB78718	2 BM08835	0 AW66062	4 CD55000	4 CA39517	0 BE53125	AA63750	AU12733	AA38892	AU12689	AA067236	0 BF88834	4 CF12556	2 BG80611	14 CA848058	3 BU05452	0 AW32045	0 BF09475	4 CF75030	4 CF12564	0 BF86833	2 BI65362	0 BF53911	2 B145295	CA75086	AULSIS	AU13034	AU134076	3 BU8448	4 CD65517	AU130700	3 BU8552	BI75390	AU11939	0 BF1600	2 BI68844
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Result No.	:							U												O																								

ALIGNMENTS

EST 25-APR-2001 AW446321 257 bp mRNA linear 84973 MARC 1BOV Bos taurus CDNA 5', mRNA sequence. AW446321 AW446321.1 GI:6988107 RESULT 1
AW446321
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS SOURCE ORGANISM

BST.
Bos taurus (cow)
Bos taurus
Bos taurus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota, Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidea; Bovinae; Bos.
1 (bases 1 to 257)

REFERENCE

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cerebellum"
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PUBMED
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                               Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
V0.980904.e. Vector identified by cross_match with the -minscore 20
pcr PRimers
Smith, T.P.L., Grosse, W.W., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, B., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY363360 RIKEN full-length enriched, 0 day neonate cerebellum Mus musculus cDNA clone C230084A06 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryotta, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Butheria, Rodentia; Sciurognathi; Muridae, Murinae, Mus. 1 (bases 1 to 305)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osaco, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yaqi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Golobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
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Library, made_from_pooled_tissue_from_lymph_node, ovary,
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                                                                                                                                                                                                                                         USDA, ARS, US Meat Animal Research Center
PO BOX 166, Clay Center, NE 68933-0166, UG
Tel: 402 762 4366
Fax: 402 762 4390
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Matches:
Conservative:
Mismatches:
Indels:
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Plate: 53 row: A column: 6
Seq primer: ATTTAGGTGACATTAG
Location/Qualificers
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                                                                                                                                                                                                                                                                                                                                                                                                                                      FORWARD: AGGAAACAGCTATGACCAT
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Best Local Similarity:
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DB:
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        AUTHORS
                                                                                                                                                           JOURNAL
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SOURCE
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                                                                                                                TITLE
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Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
Gariboldi,M., Gissi,C., Godzik,A., Graimmond,S.,
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Kawai,H.H., Kawasawa,Y. Kediterski,R.M., King,B.D., Konagaya,A.,
Kurochkin,I. Marchionni,L., McRenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan, W.J., Pertea,G., Pesole,G.,
Numata,K., Okido,T., Pavan,W.J., Pertea,G., Resole,G.,
Ravasi,T., Reed,J.C., Semple,C.A., Serou,M., Shimada,K.,
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Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
Verardo,R., Wanger,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,
Walg,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Hayatsu,N., Hirozane-Kishikawa,T., Komno,H., Nakamura,M.,
Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,
Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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Email: genome-resigned.

Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,

Alzawa, K., Akimura, T., Arakawa, T., Toth, M., Kawai, J., Konno, H.,

Hrozane, T., Imotani, K., Shisi, Y., Itoh, M., Kawai, J., Konno, H.,

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Shiraki, T., Yagami, M., Waki, K., Watahiki, D., Sato, K., Shibata, R.,

Shiraki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKRN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Exploration Rick or contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Yoshihide Hayashizaki
Laboratorry for denome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
Tel: 81-45-503-922
Fax: 81-45-503-9216
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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BY362999 RIKEN full-length enriched, adult male corpora quadrigemina Mus musculus cDNA clone B230383N06 3', mRNA sequence.
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Lydoubly Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute of Thysical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9212
Eax: 81-45-503-9212
Eax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
Will:http://genome-gsc.riken.go.jp,
Alzawa,K., Akimura,T., Arakawa,T., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Muratea,M., Nakamura,M., Nounra,K., Nunazaki,R.,
Ohno,M., Sakai,K., Sakazume,M., Sasaki,D., Sato,K., Shibata,K.,
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Ohno,M., Sakai,K., Parengami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. 'Direct Submission
Computational Analysis of Full-benome Computational Analysis of Full-trapper Computational Analysis of Full-trapper of Captraper-selected oDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence of in Mouse Genome
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence of in Mouse Genome
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dev stage="adult"
lab_host="DRIOB"
/clone_lib="RIKEN full-length enriched, adult male corpora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viote="Site 1: Sal1; Site 2: BamHI; cDNA library was propared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5].
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CONAs.
Nature 420, 563-573 (2002)
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M78197 Subtracted Hippocampus, Stratagene (cat. #936205) Homo sapiens cDNA clone HHCPQ03 similar to Fibroblast growth factor
                                                                                                         285 CACAGCCAGAIGGCTGIGCACAAGCTGGCCAAGAGCAICCCTCTGCGCAGACAGGTAACA 344
                                                                              1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(Dases 1 to 377)
Adams, M.D., Dubnick, M., Kerlavage, A.R., Moreno, R., Kelley, J.M., Neterback, T.R., Nagle, J.W., Fields, C. and Venter, J.C.
Sequence identification of 2,375 human brain genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: lambdaZAP-II; The hippocampus library (#4 above) was subtracted with a fibroblast cell line cDNA library (Stratagene cat. #936209; WISB lung fibroblast cell line; oligo-df + random primed cDNA synthesis; lambdaZAP-II vector, 1.0kb average insert size.) by the method of Sive & St. John (Nucl. Acids Res. 16:10937,
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#936205)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
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Conservative:
Mismatches:
Indels:
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/mol_type="mRNA"
/db_xref="ATC" (inhost):78796"
/db_xref="GDB:D0S1193E"
/db_xref="caxon:9606"
/clone="HHCPQ03"
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                           US-09-757-415A-3 (1-22) x AW446323 (1-343)
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Seg primer: M13 Forward.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                    receptor, mRNA sequence.
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Homo sapiens
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10. (bases 1 to 343)

11. (bases 1 to 343)

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                                                                                                                                                                                                      /organism="Bos taurus"
/mol type="mRNA"
/db_xref="taxon:9913"
/tissue type="pooled"
/lab_host="pooled"
/lab_host="DH10B"
/clone lib="MARC 1BOV"
/note="Vector: pCMV SPORT6; Site_l: Not1; Site_2: Sal1;
Libzary made from pooled tissue From lymph node, ovary,
fat, hypothalamus, and pituitary."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D 11282978
CONTECT: Smith TPL
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscor
and -minmatch 12 options.
PCR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW446323 343 bp mRNA linear
84979 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
AW446323
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Conservative:
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Plate: 53 row: B column: 6
Seg primer: ATTRAGGTGACATTAG.
Location/Qualificers
                                                                                                                                                          US-09-757-415A-3 (1-22) x BY362999 (1-327)
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Bos taurus
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                           Percent Similarity:
Best Local Similarity:
Query Match:
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Score:
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AW446323
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Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00001 row: c column: 9.
Location/Qualifiers
1.0.399
/organism="Rattus norvegicus"
/mol Type="MRNA"
/db Zref="taxon:10116"
/clone="trax1.00001-c9"
/fissue type="choried plaxus brain"
/clone="trax1.00001-c9"
/fissue type="choried plaxus brain"
/clone="trax1.00001-c9"
/note="Tector: pcAv, Site_1: Sall; Site_2: NotI; choroid plexus brain region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415 bp mRNA linear EST 16-WAY-2003
AMCONTUC:TRCP2-00003-F6-A trop2 (10289) Rattus norvegicus cDNA clone
CB800339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CB800339.1 GI:29912517
BST.
BST.
Status norvegicus (Norway rat.)
Rattus norvegicus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Site_2: NotI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA Tel: 805 447-4881
Plate: 00003 row: f column: 6.
Location/Qualifiers
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| Corganism="Rattus norvegicus" |
| / Organism="Rattus norvegicus" |
| / Organism="Rattus norvegicus" |
| / Organism="Rattus |
| / Organism="Rattus |
| / Organism="Lattices |
| / Lissue type="Choroid plexus brain" |
| / Orde="Vector: C6KFGFTL; Site_1: Sall; Sichoroid plexus brain region" |
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Amgen EST Program.
Amgen Rat. BST Program
Unpublished (2003)
Contact: Dan Fitzpatrick
Amgen, Inc
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                                                                                 397 bp mRNA linear EST 16-MAY-2003 clone trcp2-00004-D11-A trcp2 (10289) Rattus norvegicus cDNA clone trcp2-00004-d11 5', mRNA sequence.
CB772368 1 GI:29860759
EST.
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AMGNUC:TRCX1-00001-C9-A trcx1 (10261) Rattus norvegicus cDNA clone
CB706389
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
Contact: Dan Fitzpatrick
Amgen, Inc
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Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
Contact: Dan Fitzpatrick
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RESULT 9 BF922260/c LOCUS

8 g ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS

MEDLINE PUBMED COMMENT JOURNAL

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AMGNNUC: NRHY4-00054-B8-A W Rat hypothalamus (10464) Rattus norvegicus cDNA clone nrhy4-00054-b8 5', mRNA sequence. CB787182. CB787182.1 GI:29875573
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/mol_type="mRMs"
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/note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; W Rat
hypothalamus adult female Wistar rat avg. insert size 2.3
kb fraction 6 and 7"
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Bos taurus
Bos taurus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                      1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
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/mol type="mmn" sapies.
/do xref="taxon.9606"
/do ref="taxon.9606"
/clone lib="Nrg10147"
/note="Organ: nervous tumor; Vector: puc18; Site_1: Sma1; Site_2: Sma1, A min1. library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions.
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1 (Bases 1 to 419)

Dias Lo 419)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: +55-11-2704922
Email: asimpson@ludwig.org.br
This seimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NT0147-191100-483-ao6&t3=2000-11-19&t4=1)
Seq primer: puc IB forward
High quality sequence stop: 419.
                                                                                                                                                                                                                                                                          BF922260 419-JAN-2001 QVZ-NT0147-191100-483-a06 NT0147 Homo sapiens cDNA, mRNA sequence. BF922260
                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shotgun sequencing of the human transcriptome with ORF expressed sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
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EST 19-NOV-2001

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Score:

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Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Weat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4360
Fax: 402 762 4360
Fig. 1 smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
vo 980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch I options.
PCR PRimers
FORMARD: AGGAAACAGCTACACAT
BACKWARD: GTTTTCCCAGTCACCACAT
BACKWARD: GTTTTCCCAGTCACCACAT
BACKWARD: GTTTTGCGAGTCACCACTATG.
Seq primer: ATTTAGGTGACCATATAG.
Seq primer: ATTTAGGTGACCATATAG.
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Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W. Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4360
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
and -minmatch 12 options.
PCR PRIMETS.
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1 (Dases 1 to 475)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
                          Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                           Bovidae, Bovinae; Bos.

1 (Dases 1 to 474)

Smith,T-D., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F.,
Quackenbush,J. and Keelle, Dwoled-tissue normalized bovine cDNA
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
11282978
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BACKWARD: GTTTTCCCAGTCACGACG
Plate: 140 row: A column: 21
Seg primer: ATTTAGGTGACACTATAG.
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Bos taurus
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COMMENT

FEATURES

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/tissue type="RPE/choroid"
/dev_stage="RPE/choroid"
/dev_stage="RAdult"
/lab_host="EMBH10B"
/clone_lib="Human Retinal pigment epithelium/choroid cDNA
/clone_lib="Human Retinal pigment epithelium/choroid cDNA
/clone_lib="Human Retinal pigment epithelium/choroid cDNA
/un-normalized, unamplified): cs"
/note="Graga: Eye' Vector: pCWYSPORT6, Two different donor eyes (7-50 years old) yielded approximately 600 mg of dissected RPE/choroid tissue. This in turn yielded 340 ug of total RNA and 7 ug of mRNA. A directionally cloned cDNA library in the pCMYSPORT6 vector was constructed at Life Technologies (Rockville, ND; now part of Invitrogen Corp), essentially following the protocols of the SuperScript Plasmid System (Invitrogen Corp).
/thtp://www.invitrogen.com/>). The library code designation was cs. For this library cDNA inserts were cloned into the Not!/Mull sites of the vector. EST analysis was performed on the unamplified library at the NH Intramural Sequencing Center (NISC)."
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                                                                                                                                                                Wistow, G., Bernstein, S.L., Wyatt, M.K., Farris, R.N., Behal, A., Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K.
Txpressed sequence tag analysis of human RPE/choroid for the NEIBank Project: Over 6000 non-redundant transcripts, novel genes and splice variants
                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                         Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
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Mismatches:
Indels:
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Plate: 61 row: b column: 08
Seg primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. 498
/organism="Homo sapiens"
/mol_type="mRNA"
/db Zref="taxon:9606"
/clone="cs61b08"
                                                                                                                                                                                                                                                                           Mol. Vis. 8 (4), 205-220 (2002)
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                    CA395172.1 GI:24730401
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                                                              Homo sapiens (human)
                                                                                                                                                   (bases 1 to 498)
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                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 301 402 3452
Fax: 301 496 0078
                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone lib="NIA Mouse E9.5 Whole Embryo cDNA Library Long)"
             Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
133 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@1gsun.grc.nia.nih.gov
Plate: B0305 row: F column: 05
Seq primer: M13 Reverse
High quality sequence stop: 483
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
DB:
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Alignment Scores:

ORIGIN

.. No.:

RESULT 14 CA395172 LOCUS DEFINITION

g à

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EST.

Mus musculus (house mouse)

Mus musculus

Bukartyota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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S NIH-MGC http://mgc.nci.nih.gov/.

S NIH-MGC http://mgc.nci.nih.gov/.

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ibbrary constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .514
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BE531255.1 GI:9759991
mRNA sequence.
                                     ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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Length: Matches: Conservative: Mismatches: Indels: Gaps: 7.85e-07 107.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: DB:

US-09-757-415A-3 (1-22) x BE531255 (1-514)

179 CATAGCCAGATGGCTGTGCACAAGCTGGCCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 238 1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20 ò gg

21 ValSer 22

ò

239 GTGTCA 244

Search completed: August 9, 2004, 00:15:16 Job time : 618.355 secs

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1, Appli 2068, Ap 725, App

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1, Appli 5, Appli 239, Appl 1867, Ap 3, Appli 3, Appli 5655, Ap 6174, Ap 1509, Ap

Sequence

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Sequence

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APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Office, J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSED: INCTE PHARMACEUTICALS, INC.
STREET: 3174 FORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
REPLICATION CLASSIFICATION CAPPLICATION:
CLASSIFICATION:
CLASSIFICATION:
CLASSIFICATION:
CLASSIFICATION:
CLASSIFICATION:
                              US-08-070-165F-5

US-08-070-165F-5

US-08-418-5

US-08-418-5

US-08-471-570-3

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US-09-252-991A-1482

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NAME: Zeller, Karen J.
REGISTATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1288, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
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US-09-023-655-1288
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                                                                                                                                , Search time 16.7895 Seconds (without alignments) 727.177 Million cell updates/sec
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-07-997-133-2
US-08-459-296-1
US-08-451-822A-14
US-08-323-430-14
US-08-371-0011-14
PCT-US96-00331-14
US-07-631-717A-1
US-08-771-570-5
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Maximum Match 100%
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Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Result

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Sequence 10. 528855
Sequence 10. 528855
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STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: ALINGTON STADE: Virginia
STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: ALINGTON STADE: STADE: Virginia
SIP: 22202
STREET: 1855 Jefferson Davis Highway, Fourth Floor CITY: ALINGTON STADE: STADE: Virginia
SIP: 22202
SCOMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOPTWARE: PROMETTIN PARTICE STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STADES: NEEDINGTON STAD
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 28-DEC-1992

CLASSIFICATION NUMBER: US/07/642,755

FILING DATE: 18-JAN-1991

ATONEX/AGENT INPOMBER: US/07/642,755

ATONEX/AGENT INPOMBER: 24,618

REGISTRATION NUMBER: 24,618

REGISTRATION NUMBER: 24,618

REGISTRATION NUMBER: 24,618

REGISTRATION NUMBER: 24,618

REGISTRATION NUMBER: 769-226-0

TELEPHONE: (703)521-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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100.00%
                             TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2360 base pairs
                                                                                                                                                                                       TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MMEDIATE SOURCE:

LIRRARY: GENBANK

; CLONE: 231386

US-09-023-655-1288
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
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Best Local Similarity:
TELEPHONE:
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Pred. No.:
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US-004-459-296-1

Sequence 1, Application US/08459296

Patent No. 5670323

Jane No. 5670323

Jane No. 5670323

APPLICANT: No. 56703234, Michael

APPLICANT: Baird, Andrew

TITLE OF INVENTION: DISEASE

JUNERROTO: DISEASE

MUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: No. York

STATE: No. York

COMPUTER: READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: BEACABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: BEACABLE FORM:

MEDIUM TYPE: OBSECTION DATA:

APPLICANTION NUMBER: 18,812

ATTONEY/AGENT INFORMATION:

MAME: Misrock, S. Lealie

REGISTRATION NUMBER: 18,812

ATTONEY/AGENT INFORMATION:

MAME: Misrock, S. Lealie

REGISTRATION NUMBER: 18,812

REFERENCE JOCKET NUMBER: 7573-024

TELEBEHONE: 122-790-9990
                                                                                                                                                                                              Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                             US-09-757-415A-3 (1-22) x US-07-997-133-2 (1-2469)
                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                                                                           Gaps:
                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-997-133-2
                                                                                                                                                        2.04e-10
107.00
100.00%
100.00%
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LOCATION: 1...2466
OTHER INFORMATION:
LENGTH: 2469 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 212-869-864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 2469 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
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1 HisSerGlnMeralaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
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US-08-451-822A-14
US-08-451-822A-14

Sequence 14, Application US/08451822A

Sequence 14, Application US/08451822A

Sequence 14, Application US/08451822A

Sequence 14, Application

APPLICANT: Crumley, Greg

APPLICANT: Crumley, Greg

APPLICANT: Schlessinger, Joseph

TITLE OF INVENTION: Ribxoblast Growth Factor Receptors

TUTLE OF INVENTION: Ribxoblast Growth Factor Receptors

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rhone-Poulenc Rorer Legal Department

STREET: 500 Arcola Road

CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONTRY: USA

ZUP: 19426

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENI APPLICATION DATA:
APPLICATION NUMBER: US/08/451,822A
FILING DATE: 26-MA-1995
CLASSIFICATION NUMBER: US 08/323,430
FILING DATE: 14-OCT-1994
PRIOR APPLICATION NUMBER: US 07/934,372
FILING DATE: 21-AUG-1992
PRIOR APPLICATION NUMBER: US 07/934,372
FILING DATE: 21-AUG-1992
PRIOR APPLICATION NUMBER: US 07/934,372
FILING DATE: 16-OLL-199
APPLICATION NUMBER: 29-099
REPERBALCATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: 29,699
REFERENCE/DOCKET NUMBER: 29,699
REFERENCE/DOCKET NUMBER: 39,699
REFERENCE/DOCKET NUMBER: 24-3816
TELEPHONE: G100 454-3808
INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
LENGTH: 2662 DASSE PAIRS
LENGTH: 2662 DASSE PAIRS
LENGTH: 2662 DASSE PAIRS
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Matches:
Conservative:
Mismatches:
Indels:
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               US-09-757-415A-3 (1-22) x US-07-997-133-2 (1-2469)
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STRANDEDNESS: single
                                                                                                                                                                    1285 GTGTCT 1290
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Percent Similarity:
Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                      1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
US-07-997-133-2
Sequence 2, Application US/07997133
Sequence 2, Application US/07997133
Sequence 2, Application US/07997133
SEQUENCE INFORMATION:
APPLICANT: Bergonzoni, Laura
APPLICANT: Isacchi, Antonella
APPLICANT: Roncucci, Romeo
APPLICANT: Roncucci, Romeo
TITLE OF INVENTION: Extracellular Form of the Human
TITLE OF INVENTION: Fibroblast Growth Factor Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSE: P.C. STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlington STATE: Virginia ZIP: 22202
               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELBM PC compatible
COMPUTER: ELBM PC compatible
COPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/997,133
FILING DATE: 28-DEC-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/642,755
FILING DATE: 18-JAN.1991
ATPORNEY/AGENT INFORMATION:
NAME: Oblon, Norman F:
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 769-226-0
TELEPHONE: (703)521-4500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
               Length:
Matches:
Conservative:
Mismatches:
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2469 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
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Best Local Similarity:
                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
Alignment Scores:
Pred. No.:
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Sequence 14, Application US/08371001
Patent No. 5783683
GENERAL INFORMATION:
APPLICANT: Morrison Ph.D., Richard
TITLE OF INVENTION: Methods and Composition for Treating
TITLE OF INVENTION: Tumor Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                           CITY: San Diego
CITY: San Diego
CUNTRY: CA
COUNTRY: USA
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BATENIT Release #1.0, Version #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/371,001
FILING DATE: January 10, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "IDENTITY OF NUCLEOTIDE PROVISIONAL"
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                                                                                                                                                                                                                              ADDRESSEE: Gray Cary Ware & Freidenrich
STREET: 401 "B" Street, Suite 1700
CITY: San Diego
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BEOTHER, HARRIER F.
REGISTRATION NUMBER: 35,461
REFERENCE/DOCKET NUMBER: P00095USO
TELECHONICATION INFORMATION:
TELEPHONE: (619) 236-1049
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2733 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: 210.7467
OTHER INFORMATION: FGFRI Alpha Exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
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) LOCATION: 117 —

OTHER INFORMATION: "IDE

) OTHER INFORMATION: NUCL

US-08-371-001-14
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LOCATION: 57
OTHER INFORMATION: "IDE
OTHER INFORMATION: NUCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity:
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Pred. No.:
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DB:
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                               1312 CACAGCCAGATGGCTGTGCACAAGCTGGCCAAGAGCATCCCTCTGGGCAGAAGCA 1371
1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
                                                                                                                                                                                                          Sequence 14, Application US/08323430
; Patent No. 6544546
GENERAL INFORMATION:
APPLICANT: Dionne, Craig A
PAPLICANT: Crundley, Greg
APPLICANT: Crundley, Greg
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: Fibrobiast Growth Factor Receptors
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Rhone-Poulenc Rorer Legal Department
STREET: 500 Arcola Road
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,430
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US to be assigned
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/549,587
FILING DATE: 06-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Goodman, Rosanne
REGISTRATION NUMBER: 32.534
REGISTRATION NUMBER: 32.534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: A0496
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 454-3817
TELEFAX: (215) 454-3808
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                        1372 Grerer 1377
                                                                                    21 ValSer 22
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Best Local Similarity:
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US-08-323-430-14
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1342 CÁCAGCAGÁTGGCTGTGCACAAGCTGGCCAAGAGAGCATCCCTCTGCGCAGACAGGTAACA 1401
                                                                                                                                                                                                                                              1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
Length:
Matches:
Conservative:
Mismatches:
Indels:
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1372 Grérér 1377

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Sequence 1, Application US/07631717A
Patent No. 5270197
GENERAL INFORMATION:
APPLICANT: And Anner
APPLICANT: Alagsbrun, Michael
APPLICANT: Leder, Philip
TITLE OF INVENTION: SYSTEM FOR ASSAYING BINDING
TITLE OF INVENTION: FACTOR RECEPTOR
TITLE OF INVENTION: FACTOR RECEPTOR
TITLE OF INVENTION: FACTOR RECEPTOR
THE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
COUNTR: Boston
COUNTR: Boston
COUNTR: D110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/631,717A
FILING DATE: 19901220
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLIAND DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PAUL T. CLARK
REGISTRATION NUMBER: 30,162
REPRENCE/POCKET NUMBER: 00383/018001
TELECOMMUNICATION INFORMATION:
TELECHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.26e-10
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                       1402 GTGTCT 1407
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21 ValSer 22
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Best Local Similarity:
Query Match:
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Pred. No.:
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                                                                                                                                             US-07-631-717A-1
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                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 57
OTHER INFORMATION: "IDENTITY OF NUCLEOTIDE PROVISIONAL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 117 -
CTHER INFORMATION: "IDENTITY OF NUCLEOTIDE PROVISIONAL"
PCT-US96-00331-14
                                                                            Sequence 14, Application PC/TUS9600331
GENERAL INFORMATION:
APPLICANT: GENTA INCORPORATED
TITLE OF INVENTION: METHODS AND COMPOSITION FOR
TITLE OF INVENTION: TREATING TUMOR CELLS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: St. Diskette, 1.44 Mb
MEDIUM TYPE: St. Diskette, 1.44 Mb
MEDIUM TYPE: St. Diskette, 1.44 Mb
MEDIUM TYPE: St. Diskette, 1.44 Mb
MEDIUM TYPE: ST. Diskette, 1.44 Mb
MEDIUM TYPE: SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: MACA PERIECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00331
FILING DATE: 10 JANUARY 1996
CLASSIFTCATION: DATA:
APPLICATION NUMBER: 08/311,001
FILING DATE: 10 JANUARY 1995
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 218/068-PCT
FELECOMMUNICATION NUMBER: 218/068-PCT
TELEFAX: (213) 459-160
TELEFAX: (213) 455-0440
TELEFAX: (213) 455-0440
TELEFAX: 67-3510
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2733 base pairs
TYPE: Nucleic acid
STRANDEDRESS: SINGLE
TOPOLOGY: linear
MOLECULE TYPE: DNA (Genomic)
FRATURE:
FRATURE:
**MOLECULE TYPE: DNA (Genomic)
FRATURE:
**MOLECULE TYPE: DNA (Genomic)
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**MOLECULE TYPE: DNA (Genomic)
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**MOLECULE TYPE: DNA (GENOMIC)
**MOLECULE TYPE: DNA (G
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LOCATION: 210.7467
OTHER INFORMATION: FGFR1 Alpha Exon
                                                                                                                                                                                                                                                                                 ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.34e-10
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NAME/KEY: misc_feature
...artON: 117 ... "TD
                                                                                                                                                                                                                                                                                                                                                                       CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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Best Local Similarity:
Query Match:
                                                    PCT-US96-00331-14
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Oy 1 HisSerGlnWetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
Db 1500 CATAGCCACATGGCACAAGCTGGCCAAGAGCATCCCTCTGCGCAGACGACAGAGTAACA 1555
Oy 21 ValSer 22
Db 1560 GTGTCA 1565
RESULT 10
US-08-166-717D-1
; Sequence 1, Application US/08166717D
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US-09-757-415A-3 (1-22) x PCT-US96-00331-14 (1-2733)

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ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels:
                                                                          130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1954 base pairs
CORRESPONDENCE ADDRESS:
                                                                                                                      Massachusetts
: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
; LOCATION: 25..1953
US-08-471-570-5
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Query Match:
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                                                                    STREET: 130 Wa
CITY: Boston
STATE: Massach
COUNTRY: US
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                                         APPLICANT: Yayon, Avner
APPLICANT: Yayon, Avner
APPLICANT: Ornitz, David M.
APPLICANT: Clader, Philip
APPLICANT: Leder, Philip
TITLE OF INVENTION: SYSTEM FOR ASSAVING BINDING
TITLE OF INVENTION: TO A HEPARIN-BINDING GROWTH
TITLE OF INVENTION: PACTOR RECEPTOR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Bibing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08471570
Sequence 5, Application US/08471570
Patent No. 5750371
GENERAL INFORMATION:
APPLICANT: SENCO, Masabaru
APPLICANT: WATANABE, Tatsuya
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: U.S.A.

COMPUTER READABLE FORM:
MEDIUM TYPES: 3.5." Diskette, 1.44 Mb
MEDIUM TYPES: 3.5." Diskette, 1.44 Mb
MEDIUM TYPES: 3.5." Diskette, 1.44 Mb
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: WINDOWS 95
SOFWARE: WOORDEFIECT (Version 7.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/166,717D
FILING DATE: 12/14/93
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/631,717
FILING DATE: 12/20/90
ATTONNEY/AGENT INFORMATION:
NAMM: KAISTING BISKEY-BRACK
REGISTRATION NUMBER: 39,109
REGISTRATION NUMBER: 39,109
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
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TELECOMMULICATION INFORMATION:
TELECOMMULICATION 1723-4123
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107.00
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SEQUENCE CHARACTERISTICS:
LENGTH: 3503
                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1560 GTGTCA 1565
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Query Match:
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1258 AGCCAGCCGGCTGTGCACAGCTGACCCAACCTTGCCCCTGCGGAGACAGGTAACATT 1317
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Patent No. 5750371
GENERAL INFORMATION:
APPLICANT: SENOO, Masaharu
APPLICANT: SENOO, Masaharu
APPLICANT: WATANABE, Tatssuya
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CONFUNE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,570
FILING DATE: 06-UN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/149,664
FILING DATE: 16-AUG-1991
ATTORNEY/AGENT INCOMMATION:
NAME: LINEK, Exnest V
REGISTRATION NUMBER: 29622
REFERENCE/COKET NUMBER: 29827
REGISTRATION NUMBER: 29823
REFERENCE/COKET NUMBER: 29827
REGISTRATION NUMBER: 29823
REGISTRATION INFORMATION:
NAME: LINEK, Exnest V
REGISTRATION NUMBER: 29823
REFERENCE/COKET NUMBER: 29823
REFERENCE/COKET NUMBER: 29823
REFERENCE/COKET NUMBER: 29823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
Conservative:
Mismatches:
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1411 AGCCAGCCGGCTGTGCACAAGCTGACGAACGTATCCCCCTGCGGAGACAGGTAACAGTT 1470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dionne, Craig A
APPLICANT: Crumley, Greg
APPLICANT: Jaye, Michael
APPLICANT: Jaye, Michael
APPLICANT: Jaye, Michael
APPLICANT: Jaye, Michael
APPLICANT: Jaye, Michael
APPLICANT: Jaye, Michael
APPLICANT: Jaye, Michael
APPLICANT: Jebroblast Growth Factor Receptors
NUMBER OF SEQUENCES: 15
ADDRESSED: Rhone-Poulenc Rorer Legal Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Rhone-Poulenc Rorer Legal Department STREET: 500 Arcola Road CITY: Collegeville
                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERALING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,822A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                      FILING DATE: 26-MAY-1955
CLASSIFICATION: 435
PROGA SPPLICATION 1435
PRIOR APPLICATION NUMBER: US 08/323,430
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/934,372
FILING DATE: 21-AUG-1992
PRIOR APPLICATION NUMBER: US 07/934,372
APPLICATION NUMBER: US 07/934,372
FILING DATE: 06-UUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                     NUMBER: US/08/451,822A
26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: SAVIZAY, MATTIN
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: 20,699
REFERENCE/DOCKET NUMBER: 20,699
TELEPRANCE/DOCKET NUMBER: 30,96E
TELEPRANCE (610) 454-3816
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 3416 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application US/08323430 Patent No. 6344546 GENERAL INFORMATION:
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83.00
85.71%
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ZIP: 19426
COMPUTER READABLE FORM:
              ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linea
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-323-430-15
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Sequence 15. Application US/08451822A
Fatent No. 586388
GENERAL INFORMATION:
GENERAL INFORMATION:
FAPPLICANT: Crumley, Greg
APPLICANT: Crumley, Greg
APPLICANT: Crumley, Greg
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: Fibroblast Growth Factor Receptors;
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Legal Department
STREET: S00 Arcola Road
CITY: Collegeville
STATE: PA
                                                                              ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPOTER: ABC COMPATIBLE
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,570
FLING DATE: 06-4UN-1995
CLASSIFICATION NUMBER: US/08/149,664
FILING DATE: 106-AUG-1991
APPLICATION NUMBER: US/08/149,664
FILING DATE: 16-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: LINEK, ETNEST V
REGISTRATION NUMBER: 2982022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 2676 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.00
85.71%
85.71%
77.57%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                          Massachusetts
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Best Local Similarity:
Query Match:
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                  Boston
                                                                  ns
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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US-08-471-570-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22
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us-09-757-415a-3.p2n.rni

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TELECOMMUNICATION INFORMATION:
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APPLICANT: Poulin, Matthew L
TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ing-Ming Chiu
STREET: 910 Avenue
STREET: 910 Avenue
CITY: Columbus
STATE: Ohio
                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTUMEN: APPLICATION DATA:
PSPLICATION NUMBER: US/08/323,430
FILING DATE:
FILING DATE:
PPLICATION NUMBER: US to be assigned
FILING DATE:
PRICATION NUMBER: US 07/549,587
FILING DATE: 21-AUG-1992
APPLICATION NUMBER: US 07/549,587
FILING DATE: 06-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: GOOGNAIN, ROSAINE
REGISTRATION NUMBER: 32,534
REGISTRATION NUMBER: 32,534
REGISTRATION NUMBER: 32,534
REGISTRATION NUMBER: 32,534
REGISTRATION NUMBER: 32,534
REGISTRATION NUMBER: 32,534
REGISTRATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LEMETHER CHARACTERISTICS:
LEMETHER CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/070,165F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.18e-05
83.00
85.71%
85.71%
Floppy disk
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CLASSIFICATION: 435
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Best Local Similarity:
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STRANDEDNESS:
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MEDIUM TYPE:
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Pred. No.:
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DB:
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1279 AGCCCACCCGCTGTGCACAAGCTGAGCAAGAGTCTCCCCCTGCGCAGACAGGGTAACAGTG 1338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE: Nucleotide sequences of two newt
TITLE: (No. 57503650phthalmus viridescens) fibroblast growth
TITLE: factor receptor-2 variants
JOURNAL: Biochim. Biophys. Acta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 1 TO 2675
US-08-070-165F-5
                                                                                                                                                                                                                                             ONGANISM: No. 5750365ophthalmus viridescens
ONGANISM: No. 5750365ophthalmus viridescens
DEVELOPMENTAL STAGE: Adult
TISSUE TYPE: Regenerating forelimb blastema
CELL TYPE: Mesenchyme and Epithelium
IMMEDIATE SOURCE:
LIBRARY: lambda gt11
CLONE: KP23-1
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-757-415A-3 (1-22) x US-08-070-165F-5 (1-2675)
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TELEPHONE: (644)-293-8093
TELEPAX: (614)-293-5631
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2675 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: 3'UTR
LOCATION: 2512.2675
PUBLICATION INFORMATION:
AUTHORS: POULIN, Matthew L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.04e-05
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90.48%
80.95%
75.70%
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325..2511
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Job time: 23.7895 secs
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LOCATION: 1..324
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
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LOCATION:
FEATURE:
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Sequence 98, Appl
Sequence 41, Appl
Sequence 271, Appl
Sequence 271, Appl
Sequence 182, Appl
Sequence 182, Appl
Sequence 380, Appl
Sequence 380, Appl
Sequence 380, Appl
Sequence 380, Appl
Sequence 380, Appl
Sequence 382, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 25, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 28, Appl
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Sequence 29, Appl
Sequence 29, Appl
Sequence 29, Appl
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Sequence 28, Appl
Sequence 29, Appl
Sequence 132, Appl
Sequence 29, Appl
Sequence 132, Appl
Sequence 132, Appl
Sequence 132, Appl
Sequence 132, Appl
Sequence 132, Appl
Sequence 133, Appl
Sequence 133, Appl
                                              Sequence 1, Appli
Sequence 7, Appli
Sequence 3, Appli
Sequence 299, App
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Sequence 15, Appl
Sequence 21359, A
Sequence 36, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cocks, Benjamin G.
Stuart
Susan G. Stuart
Jeffrey J. Schlamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-954-556-3
US-09-968-007A-461
US-10-68-007A-461
US-10-19-820-78
US-10-087-192-1130
US-10-087-192-1129
US-10-087-192-1129
US-09-954-556-13
US-09-954-556-13
US-10-282-125-1359
US-10-282-125-1359
US-10-282-122A-21359
US-10-99-954-56-13
US-10-641-643-1288

US-10-307-817-5

US-10-307-817-3

US-10-307-817-3

US-10-307-817-3

US-10-307-817-3

US-10-307-817-3

US-10-101-510-299

US-10-299 812-41

US-10-004-988-271

US-10-007-926-712

US-10-007-926-712

US-10-007-926-712

US-10-007-926-712

US-10-007-926-712

US-10-007-926-712

US-10-007-192-383

US-10-0087-192-383

US-10-0087-192-382

US-10-0087-192-382

US-09-916-956-56-10

US-09-954-556-10

US-09-954-556-10

US-09-954-556-10

US-09-954-556-10
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ADDRESSE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-954-456-293
US-09-954-456-1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1288, Application US/10641643 Publication No. US20040077003A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
    1978
2079
2079
57561
126266
132762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94304
    US-10-641-643-1288
    Command line parameters:
-MODEL=frame+ p2n. model - DEV=x1h
-MODEL=frame+ p2n. model - DEV=x1h
-MODEL=frame+ p2n. model - DEV=x1h
-DEPUDISHE(Applications_NA - QFWT=fasEap - SUFFIX=p2n. Tmpb - MINMATCH=0.1
-DEPUDISHE(Applications_NA - QFWT=fasEap - SUFFIX=p2n. Tmpb - MINMATCH=0.1
-LOOPECL= 0 - LOOPEXTA - START=1 - START=1 - STAR=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TSNE=1 - TS
                                                                                                                                  August 8, 2004, 23:07:35; Search time 98.5658 Seconds (without alignments) 1094.387 Million cell updates/sec
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1: /cgn2_6/ptodata/1/Pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/Pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/Pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/Pubpna/US06_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/Pubpna/US06_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/Pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/Pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/Pubpna/US08_NEW_PUB.seq:*

10: /cgn2_6/ptodata/1/Pubpna/US08_NEW_PUB.seq:*

10: /cgn2_6/ptodata/1/Pubpna/US08_NEW_PUB.seq:*

11: /cgn2_6/ptodata/1/Pubpna/US08_NEW_PUB.seq:*

12: /cgn2_6/ptodata/1/Pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/Pubpna/US09_NEW_PUB.seq:*

14: /cgn2_6/ptodata/1/Pubpna/US09_NEW_PUB.seq:*

15: /cgn2_6/ptodata/1/Pubpna/US09_NEW_PUB.seq:*

16: /cgn2_6/ptodata/1/Pubpna/US09_NEW_PUB.seq:*

16: /cgn2_6/ptodata/1/Pubpna/US09_NEW_PUB.seq:*

16: /cgn2_6/ptodata/1/Pubpna/US00_NEW_PUB.seq:*

16: /cgn2_6/ptodata/1/Pubpna/US00_NEW_PUB.seq:*

17: /cgn2_6/ptodata/1/Pubpna/US00_NEW_PUB.seq:*

18: /cgn2_6/ptodata/1/Pubpna/US00_NEW_PUB.seq:*

19: /cgn2_6/ptodata/1/Pubpna/US00_NEW_PUB.seq:*

19: /cgn2_6/ptodata/1/Pubpna/US00_NEW_PUB.seq:*
    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                             OM protein - nucleic search, using frame_plus_p2n model
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SUMMARIES

Query Match Length DB

Score

Result

of hits satisfying chosen parameters: 3222919 segs, 2451570024 residues

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Searched:

length: 0 length: 2000000000

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Minimum DB R

US-09-757-415A-3

Perfect score:

Title:

<u>:</u>

Sequence:

0.5

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Egapop 6.0 , Fgapext Delop 6.0 , Delext

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Scoring table:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Jatabase :

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US-09-757-415A-3 (1-22) x US-10-307-817-5 (1-2470)
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LOCATION: (116)..(2581)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CORGANISM: Homo sapiens
US-10-204-041-1
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ORGANISM: Homo sapiens
                                                                                                                                                 1139 Grdrcr 1144
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LENGTH: 2662
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US-10-204-041-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Agee et al.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE REFERENCE: 21402-502C
CURRENT APPLICATION NUMBER: US/10/307,817
CURRENT FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 682
SOFTWARE: CuraSequist version 0.1
LENGTH: 2470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: «UNKnown»
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: «UNKnown»
FILING DATE: «UNKnown»
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REGISTRATION NUMBER: 37,071
REGISTRATION NUMBER: 97,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMUNICATION INFORMATION:
TELEPRAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1288:
SEQUENCE CHARACTERISTICS:
LENGTH: 2360 base pairs
TYPE: NUCLEIC acid
STRANDEDNESS: single
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SEQUENCE DESCRIPTION: SEQ ID NO: 1288 ;
US-10-641-643-1288
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Publication No. US20040058338A1
GENERAL INFORMATION:
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107.00
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; NAME/KEY: CDS
; LOCATION: (116)..(2320)
US-10-307-817-5
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Best Local Similarity:
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Query Match:
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Pred. No.:
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Sequence 1, Application US/10204041
| Publication No. US20030176443A1
| Publication No. US20030176443A1
| Publication No. US20030176443A1
| GENERAL INFORMATION:
| APPLICANT: SALASSIDIS, KONSTADINOS
| APPLICANT: BALASSIDIS, KONSTADINOS
| APPLICANT: BALASSIDIS, KONSTADINOS
| APPLICANT: BALASSIDIS, KONSTADINOS
| APPLICANT: MULLER, STEFAN
| TITLE OF INVENTION: Infections and Prion Diseases
| TITLE OF INVENTION: Infections and Prion Diseases
| FILE REFERENCE: AXM-007.1P US
| CURRENT APPLICATION NUMBER: US/10/204,041
| CURRENT PLING DATE: 2002-08-16
| PRIOR APPLICATION NUMBER: PCT/EP02/05420
| PRIOR FILING DATE: 2002-06-16
| PRIOR FILING DATE: 2002-06-16
| NUMBER OF SEQ ID NOS: 20
| SOFTWARE: PATENTIN VERSION 3.1
                                                               reeccaaeaecarcccrcrececaeacaearaaca 1138
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1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgGrgGlnValThr 20
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Publication No. US20040058338A1
GENERAL INFORMATION
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME FILE REFERENCE: 21402-502C
CURRENT APPLICATION NUMBER: US/10/307,817
CURRENT FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 682
SOFTWARE: CuraSequist version 0.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
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Length:
Matches:
Conservative:
Mismatches:
Indels:

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US-09-757-415A-3 (1-22) x US-10-101-510-299 (1-3328)
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107.00
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100.00%
; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 299; LENGTH: 3328
                                              TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-299
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Percent Similarity:
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ORGANISM: HUMAN
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/10307817
Publication No. US20040058338A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFRENCE: 21402-502C
CURRENT APPLICATION NUMBER: US/10/307,817
CURRENT FILING DATE: 2002-12-02
NUMBER OF SEQ ID NOS: 682
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 3
LENGTH: 2737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 299, Application US/10101510
Publication No. US20030148295A1
GENERAL INFORMATION:
APPLICANT: WAN, JACKSON
APPLICANT: WANG, YIXIN
TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
FILE REFERENCE: 15117.0012
CURRENT APPLICATION NUMBER: US/10/101,510
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR APPLICATION NUMBER: 2001-03-20
NUMBER OF SEQ ID NOS: 805
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; LOCATION: (116)..(2587)
US-10-307-817-3
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ORGANISM: Homo sapiens
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US-10-101-510-299
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Pred. No.:
                                    Alignment Scores:
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   JS-10-307-817-7
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1180 cacadeceadardecrerecidaderedeceaadadecarcecreredecadadadanaea 1239
                          1180 CACAGCCAGATGGCTGTGCACAAGCTGGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1239
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1 HisserGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr
                                                                                                                                                                                                                                          Sequence 98, Application US/10283975A
Sequence 98, Application US/10283975A
Publication No. US20040110792A1
GENERAL INFORMATION:
APPLICANT: Ortho-Clinical Diagnostics, Inc.
TITLE OF INVENTION: Methods For Assessing and Treating Leukemia
FILE REPERENCE: CDS 293 PCT
CURRENT APPLICATION NUMBER: US/10/283,975A
CURRENT FILING DATE: 2002-10-30
PRIOR APPLICATION NUMBER: 60/340,938
PRIOR PLING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/340,081
PRIOR PLING DATE: 2001-10-30
PRIOR PLING DATE: 2001-10-30
PRIOR PLING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/341,012
PRIOR APPLICATION NUMBER: 60/341,012
PRIOR PLING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 900
SOFTWARE: Patentin version 3.1
SEQ ID NO 98
LENGTH: 3328
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US-10-302-812-41
'Sequence 41, Application US/10302812
'Publication No. US20040087016A1
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Pred. No.:

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1051 cacadecadardderdrachaacradecaadaddarcerereegagagaaaa 1110
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                                                                                      Sequence 2.1. Application US/09925302

Sequence 2.1. Application US/09925302

Patent No. US20020044941A1

GENERAL INFORMATION:

APPLICANT: ROSEN et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA104

CURRENT APPLICATION NUMBER: US/09/925,302

CURRENT FILING DATE: 2001-08-10

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 896

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 271

LENGTH: 3726
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Sequence 271, Application US/09925302

Publication No. US20030064072A9

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA104

CURRENT APPLICATION NUMBER: US/09/925,302

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US/00/05918

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR APPLICATION NUMBER: 00/124,270

PRIOR APPLICATION NUMBER: 00/124,270

SOFTWARE: PALENT US: 896

SOFTWARE: PALENTIN VEY: 2.0
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Matches:
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FEATURE:
NAME/KEY: misc feature
LOCATION: (2586)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (3523)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (3664)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (3684)
LOCATION: (3687)
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ORGANISM: Homo sapiens
     1138 GTGTCT 1143
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                                                                               US-09-925-302-271
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| Sequence 48, Application US/10044090
| GENERAL INFORMATION:
| APPLICANT: Olga Bandman
| TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
| FILE REFERENCE: PA-0028 US
| CURRENT APPLICANTION UNMBER: US/10/044,090
| CURRENT FILING DATE: 2002-01-09
| NUMBER OF SEQ ID NOS: 850
| SEQ ID NO 48
| LINE FILE FOR THE PROGRAM
| SEQ ID NO 48
| LINE FILE FOR THE PROGRAM
| SEQ ID NO 48
| LINE FILE FOR THE PROGRAM
| SEQ ID NO 48
| LINE FILE FOR THE PROGRAM
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GENERAL INFORMATION:
APPLICANT Keating et al.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CELL DEDIFFERENTIATION AND
TITLE OF INVENTION: TISSUE RECENERATION
FILE REFERENCE: HYDR-P02-004
CURRENT APPLICATION NUMBER: US/10/302,812
CURRENT FILING DATE: 2002-11-21
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PALCHIN Version 3.1
SEQ ID NO 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1228 CACAGCCAGATGGCTGTGCACAAGCTGGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature;
CTHER INFORMATION: Incyte ID No. US20020137081A1 493848CB1;
NAME/KEY: unsure;
LOCATION: 2, 9, 16, 39, 42, 68, 143, 268;
CTHER INFORMATION: a, t, c, g, or other
US-10-044-090-48
                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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107.00
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                                                                                                                                                                                                                                                  LENGTH: 3343
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1288 GTGTCT 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 Valser 22
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Best Local Similarity:
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Pred. No.:
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21 ValSer 22 ||||||

Query Match:

us-09-757-415a-3.p2n.rnpb

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US-09-757-415A-3 (1-22) x US-10-007-926A-182 (1-4066)
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 182, Application US/10007926A

Publication No. US20030149539A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BERTUCCI, FRANCOIS
APPLICANT: BERTUCCI, FRANCOIS
APPLICANT: BITRABADA, DAMIEL
APPLICANT: WOU'FEN CATHERINE
APPLICANT: VIENS, PATRICE
APPLICANT: VIENS, PATRICE
APPLICANT: WOU'FEN CATHERINE
APPLICANT: WOU'FEN CATHERINE
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APPLICANT: WOU'FEN CATHERINE
APPLICANT: WO'FEN CATHERINE
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 468
SOFTWARE PATENTIN VEY. 2.1
SEQ ID NO 182
LENGTH: 4066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1051 CACAGCCAGATGGCTGTGCACAAGCTGGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 1110
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CHER INFORMATION: fibroblast growth factor receptor 1
CTHER INFORMATION: (fms.related tyrosine kinase 2, pfeiffer syndrome)
CTHER INFORMATION: (FGFR1) gene.
US-10-007-926A-182
                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                PEATURE:

NAME/KEY: misc feature

LOCATION: (2586)

OTHER INFORMATION: n equals a,t,g, or

NAME/KEY: misc feature

LOCATION: (3523)

OTHER INFORMATION: n equals a,t,g, or

NAME/KEY: misc feature

LOCATION: (3664)

OTHER INFORMATION: n equals a,t,g, or

LOCATION: (3687)

LOCATION: (3687)

US-09-925-302-271
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ORGANISM: Homo sapiens
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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US-10-159-56-305

### Squence 305, Application US/10159563

### Squence 305, Application US/10159563

### Squence 305, Application No. US200400091541

### GENERAL INFORMATION:
### APPLICANT: Khan, Javed

### APPLICANT: Ringner, Markus

### APPLICANT: Ringner, Markus

### APPLICANT: Ringner, Markus

### APPLICANT: Ringner, Markus

### APPLICANT: Peterson, Caraten

### APPLICANT: Mclazer, Paul

### TITLE OF INVENTION: BLECTIONS OF GENES AND METHODS OF USING THE SAME FOR

### TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS

### TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS

### CURRENT FILING DATE: 2002-12-09

### PRIOR PILING DATE: 2002-12-09

### PRIOR PILING DATE: 2002-04-25

### NUMBER OF SEQ ID NOS: 444

### SEQ ID NO 305

### LEATTH: 4066

### LEATTH: 4066
                                                 1951 CACAGCCAGATGGCTGTGCACAAGCTGGCCAAGAGCATCCCTCTGCGCAGACAGGTAACA 2010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1951 CACAGCCAGATGGCTGTGCACAAGCTGGCCAAAGAGCATCCCTCTGCGCAGACAGGTAACA 2010
1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 HisSerGlnMetAlaValHisLysLeuAlaLysSerIleProLeuArgArgGlnValThr
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NAMEXKEY: misc feature

LOCATION: (1). 7(4628)

OTHER INPORMATION: any n = a,c,g,t any unknown or other
US-09-805-020-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4066
22
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Sequence 11, Application US/09805020
Publication No. US20020086384A1
GENERAL INFORMATION:
TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES
TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES
CURRENT APPLICATION NUMBER: US/09/805,020
CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 11
SEQ ID NO 11
SEQ ID NO 11
SEQ ID NO 11
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Matches:
Conservative:
Mismatches:
Indels:
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; ORGANISM: Homo sapiens
US-10-159-563-305
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                                                                                                                                          2011 GTGTCT 2016
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                                                                                                      21 ValSer 22
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Best Local Similarity:
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21 ValSer 22 ||| 1342 GAAAGT 1347

US-09-757-415A-3 (1-22) x US-10-087-192-380 (1-1726)

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WESULT 15
US-10-087-192-380
Sequence 380, Application US/10087192
Sequence 380, Application US/10087192
Sequence 380, Application US/10087192
SERMERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Elic K.
TITLE OF INVENTION: OVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: OVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: OVEL COMPOSITIONS AND METHODS FOR STILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SEQ ID NO 380
SEQ ID NO 380
SEQ ID NO 380
TYPE: DIA
CREANISM: Mus musculus
US-10-087-192-380
            Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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               2.04e-09
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Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
Query Match:
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Alignment Scores:
Pred. No.:
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Pred. No.:
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